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Title:
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           Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
           Score
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Match Length DB
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ALIGNMENTS

CDS	source	FEATURES		JOURNAL	TITLE	AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX148306	RESULT 1
<pre>/organism="Arabidopsis thaliana" /db_xref="taxon:3702" 11800 /note="unnamed protein product"</pre>	11800	Location/Qualifiers	Riken (JP)	Patent: EP 1116794-A 5 18-JUL-2001;	Transgenic plants carrying neoxanthin cleavage enzyme gene	Iuchi, S., Kobayashi, M. and Shinozaki, K.	1 (bases 1 to 1800)	Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Arabidopsis thaliana	thale cress.	•	AX148306.1 GI:14347193	AX148306	Sequence 5 from Patent EP1116794.	AX148306 1800 bp DNA linear PAT 08-JUN-2001		

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BASE COUNT
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1440	.caactcgccgtccgatcatctccaacgaagatcaacaagtcaacctcgaagcagggat	Qy
1380	1321 TCTGACGAGAATCTCAAGAGTGTCCTGTGTGAAATCCGCCTGAATCTCAAAACCGGTGAA	망
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1320	1261 ACAGATGAAGTCGTGATAGGGTCCTGTATGACTCCACCAGCTCAATTTTCAACGAG	ρЬ
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1260	1201 TGGATTGATGCTCCAGATTGCTTCTGCTTCCATCTCTGGAACGCTTGGGAAGAGCCAGAA	В
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Direct Submission
Submitted (22-APR-1999) Satoshi Iuchi, RIKEN, Plant
3-1-1 Kouyadai, Tsukuba 305-0074, Japan
(E-mail:iuchi@rtc.riken.go.jp, Tel:81-298-36-4359)
Location/Qualifiers
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Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 3869)
1 uchi.S., Kobayashi,M. and Shinozaki,K.
Characterization of neoxanthin cleavage enzyme from Arabidopsis
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FEATURES	MEDLINE REFERENCE AUTHORS TITLE JOURNAL COMMENT	RESULT ABO28617/c LOCUS DEFINITION ACCESSION WERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE	621 451 681 511 741 771	1441 3271 1501 3331 1561 3391
Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/crail-1.3/), GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlini.zool.iastate.edu/cgl-bin/sp.cgl). Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl-edu/eddy/tRNAscan-SE/). This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is MLN21 and the 3' clone is MIE1.	E 20277480 E 20277480 E 2 (bases 1 to 52232) E 2 (bases 1 to 52232) S Sato,S., Nakamura,Y., Kaneko,T., Kato,T., Asamizu,E. and Tabata,S. S Instituted (09-JUN-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934) Address for correspondence: kaos@kazusa.or.jp For the latest information on annotation of this clone, please see	AB028617 AB028617 AB028617 AB028617 AB028617 AB028617 AB028617 AB028617 AB028617 AB028617.1 GI:5041970 Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui P1 clone:MOA2. Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (sites) Sato,S., Wakamura,Y., Kaneko,T., Katoh,T., Asamizu,E. and Tabata,S. Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty P1 and TAC clones	gaagacgaaggatacatcctcttttctgttcacgacgagaaatcgagatta 1680	
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VLDDFWSESDOSWESFQVAFTDAEEGSKIVLTTRSEIVSTVAKAEKIYOMKLMTNEEC
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CDS

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CDS

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CQLHYIQELKDLTKWWKELDLASKLPYIRDRIVEVYFGALALYFEPRYSLGRIIVTKI
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FIMTWNTHQYSRSIRGCCEIKKKKKVVLCSLLIHRYSNYSLVHVLRCFVFLYNSIFLC
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Spermatophyta; Magnoliophyta; eudicotyledons; core e
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                                                                                                                                                                                                                                                                                                                                                                                        Yamada, K., Banh, J., Banno, F., Dale, J.M., Goldsmith, A.D., Lee, J. Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Boweer, L., Carninci, P., Chen, H., Cheuk, R., Yu, S., Boweer, L., Carninci, P., Chen, H., Karlin-Neumann, Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tracy, S.E., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                           Submitted (12-SEP-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94/710, USA RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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COMMENT

TITLE

Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIS. sequencing and annotation of the RAFL cDNAs: Yamada,K., Banh,J., Banno,F., Dale,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Yamamura,Y., Yu.G., Yu.S., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tracy,S.E., Davis,R.W., Ecker,J.R. and Theologis,A. ç

FEATURES

gene

5'UTR source /product="putative 9-cis-epoxycarotenoid dioxygenase"
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gcacacggaaccggtgtagctaacgccggtttggtctatttcaatggccggttattggct 780
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1923...2331
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/note="not present in ge
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1922	CCGTACGGATTTCACGGTACATTCATCGGAGCCGATGATTTGGCGAAGCAGGTCGTGTGA	1863	Db
1800	ogtacggatttcacggtacattcatcggagccgatgatttggcgaagcaggtcgtgtg	74	Qy
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1682	CTCAGGATTCGCTAAAGTTGATCTCACTGCTGGAGAAGTTAAGAAACA	Ō	ДD
1560	ggcctaaagtctcaggattcgctaaagttgatctcactactggagaagttaagaaac	G	Qy
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1262	CAAGTCGTTTTCAAGCTGCCGGAGATGATCCTCGGTGGGTCTCCGGTGGTTTACGACAAG		Db
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1020	aatacttccgattctcaccggacgaactaaatcaccggacgtcgagattcagcttga	961	Qy
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1022	GTTGGTCGGTTCGATTTTGATGGACAATTAGAATCCACAATGATTGCCCCACCCGAAAGTC	963	ДD
900	ttggtcggttcgattttgatggacaattagaatccacaatgattgcccacccgaaagt	841	Qy
962	ATGTCGGAGGATGATTTACCTTACCAAGTTCAGATCACTCCCAATGGAGATTTAAAAACC		DЪ
840	tgtcggaggatgatttaccttaccaagttcagatcactcccaatggagatttaaaaac	781	Qy
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REFERENCE
AUTHORS
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Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C.,
Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N.,
Howling, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J.,
Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H.,
Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M.,
Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
Direct Submission
AL Department of Biology, University of Pennsylvania, 38th and
Hamilton Walk, Philadelphia, PA 19104-6018, USA
C. Loases 1 to 95769
Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q.,
Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C.,
Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N.,
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Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M.,
Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
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AC013430.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (07-FEB-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Str Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
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Shinn,P., Altafi,H., Bei,Q., Chin,C., Chiou,J., Choi,E., Conn
Conway,A., Gonzales,A., Hansen,N., Howng,B., Koo,T., Lam,B.,
Lee,J., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S., Mukharsky,N.,
Nguyen,M., Palm,C., Pham,P., Sakano,H., Schwartz,J., Southwic
Thaveri,A., Toriumi,M., Vaysberg,M., Yu,G., Federspiel,N.A.,
Theologis,A. and Ecker,J.R.
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Ecker, J.R.
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1 (bases 1 to 95769)
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/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             2000 this sequence version replaced
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BAC F3F9 from chromosome
                                                                                                                                                                                                                                                                                                                                                gi:6921155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ., Khan, S., Kim, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Southwick, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Street and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conn, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QRIAPLTCLIDNEDERLYEEFTWSEYKNSTYNSRLSDNRLQQFERKTIKNLLN" complement(join(15755. .16715,16810. .16829))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INHGVSAELVSVLEHETVDFFSLPKSEKTQVAGYPFGYGNSKIGRNGDVGWVEYLLAN
ANHDSGSGPLFPSLLKSPGTFRNALESTTTSVEKMFFDVLEKITDGLGIXPRNYLSKL
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NDGSWISVPDHTSFFFNVGDSLQVMTNGRFKSVRHRVLANCKKSRVSMIYFAGPSLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MEAALSIFKLSFLLTLLSGGSDLIDSLPPNCNRAECPSYEVVHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="metglniiklslcvslvvvgsyaqapapwnpsngfrpgtcdhye
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                                                                                                                                                                                                                                   SEQCGSMEKHFAGRFVGSPGMADDSDDGSGKRKSSGKKMFGDLWKKKGQK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAF71795.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVSIVTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELKASLQGTVWAKAIEKSRETGGVGSAWAYTVAQFSWPFQWSQRVNEIWFPFEMEDEE
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/codon <pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="mGHVQLLTPCFYSFPFFSFFLLFFLFNAKNVFILISVDLTVGTV
FELEAKVEQVIPPVKVEDGESTTHETRRMRYGEEFLSSRLCRPPMVTGLEKSLDLSSS
                                                                                                                                                                                                                                                                              ESNETTAKLKKKLESVEEAKETLEAEMKKLKVQTEQWRKAADAAAVLSGGVEMNGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(13444.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(7138. .7400,7491.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to dioxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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                                                                                                   . 21156))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .13814,13956. .14310,14399.
protein; similar and gb|AA586078.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein"
              r to
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                                                                                                                                                                                        .19833,
                                               gb|T41672.1,
                                                                                                                                                                                    .20164
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Query Match
Best Local Similarity
Matches 1139; Conserv
                                                                   34107
                                                                                                                                                                                                                                                                                                  33987
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                                                                                                                       362
                                                                                                                                                                                                                                        305
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      422
                                                             TCCAAATAGCCGGGAACTTCTTCCCGGTACCGGAGAAACCTGTCGTGCATAACCTTCCGG
                                                                                                                                                                                                         gtttccttgtcagccacgag---aagctacacccgcttcctaaaacggctgatcctagtg
                                                                                                                                                                                                                                                                                                                          acactaaacagatgaatttgttccagagagcggcggcggcggcggcttggacgcggggggg
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                                                                                              ttcagatcgccggaaattttgctccggtgaatgaacagcccgtccggcgtaatcttccgg
                                                                                                                                                                              ACGCCATGATCTCACACGAGCGCCGCCGTCATCCCCATCCTAAAACGGCGGATCCTGCCG
                                                                                                                                                                                                                                                                                            AGAATCCAAAATTAAACCCGGTGCAGAGAACCGCCGCTATGGTTTTAGACGCGGTGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33566. .35539
/note="similar to 9-cis-epoxycarotenoid gb|AAF26356.1"
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GTSNGVRIKTWPSPGEENLYSNFLFKNLQMIDVGSFNVQLFNINIVHRGRDGPATS
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LMGFFFYSSLIFMRCPECKTPNYAVETRGVKSKEEKGIEQVEDGRVIEAKIRWRQKE
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COMPLEMENT (1010 (22808 . 2363,23118 . 23244,23511 . 23706))
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Tgdletsgrvdfdqqlkstmiahpkidpetrelfalsydvvskpylkvfrftsdgeks
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join(26752. .26907,27020. .27871,27923. .28153)
note="similar to expolygalacturonase precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp|Q00293|PGLX_ASPTU"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MGNKLGRKRQVVEERYTKPQGLYVNKDVDVKKLRKLIVESKLAP/
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/evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                        47.9%;
73.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 862.8; DB 8;
Pred. No. 2.1e-245;
0; Mismatches 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95769;
                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                    421
      481
                                                                                                                                                                           34106
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               ACTCCTCTTCTTCAACTTCCAAGTGGAATTTAGTGCAGAAAGCAGCAGCAATGGCTT
                                                                     CTTCAAATTATCAAACACCAAAGAATAATACAATTTCACACCCAAAACAAGAAAACAACA
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Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Iuchi,S., Kobayashi,M. and Shinozaki,K.
Transgenic plants carrying neoxanthin cleavage
Patent: EP 1116794-A 15 18-JUL-2001;
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//COGOL_Start=1
//Protein_id="CAC41199.1"
//db_xref="G1:14347204"
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IGELHGHSGIARLMLFYARGLFGLVDHSKGTGVANAGLVYFNNILLAMSEDDLPYHVK
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ILDKYAKDGSDLKWVEVPDCFCFHLWNAWEEAETDEIVVIGSCMTPPDSIFNECDEGL
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VSGFAKVNLFTGEVEKFIYGDNKYGGEPLFLPRDPNSKEEEDDGYILAFVHDEKEWKSE
LQIVNAMSLKLEATVKLPSRVEVFGFHGTFINANDLANQA"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Solanales; Solanaceae; Solanum;
                                                                         Direct Submission
Submitted (09-JAN-1998) Burbidge A., The University of Physiology and Environmental Science, Sutton Bonington Loughborough, Leicestershire, LE12 SRD, UK
On Jan 13, 1998 this sequence version replaced gi:22431
                                                                                                                                                                                                                                                                     Burbidge,A., Grieve,T.M., Jackson,A., Thompson,A. and Taylor,I.B. Structure and expression of a cDNA encoding a putative neoxanthin cleavage enzyme (NCE) isolated from a wilt-related tomato (Lycopersicon esculentum Mill.) library J. Exp. Bot. 47, 2111-2112 (1997)
                                                                                                                                                                         Direct Submission
Submitted (01-JUL-1997) Burbidge A., The University of Physiology and Environmental Science, Sutton Bonington Loughborough, Leicestershire, LE12 5RD, UK
Revised by [3]
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Matches 1134; 170 ctccagctcttcatttccctaagcaatcatcaaactctcccgccattgttgttaagccca 229 Similarity Conservative 45.8%; 0; Score 824.6; DB 8; Pred. No. 2.6e-234; 0; Mismatches 489; Indels Length 6, Gaps

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                potato.
Solanum tuberosum
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Solanum tuberosum mRNA
dioxygenase (ncedl gene
                                         AJ276244.1 GI:7209268
9-cis-epoxycarotenoid
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Spermatophyta; Magnoliophyta; eudicotyledons; or Asteridae; euasterids I; Solanales; Solanaceae; losaes 1 to 2164)
Burbidge, A., Taylor, I.B. and Thompson, A.
Potato putative 9-cis-epoxycarotenoid dioxygenas
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67 a 437 c 433 g 627 t
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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Transgenic plants carrying neoxanthi
Patent: EP 1116794-A 11 18-JUL-2001;
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Submitted (16-JUL-1999) Satoshi Iuchi, RIKEN, Plan 3-1-1 Kouyadai, Tsukuba 305-0074, Japan (E-mail:luchi@rtc.riken.go.jp, Tel:81-298-36-4359)
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NFLQKAAATALDLVETALVSHERKHPLPKTADPRVQIAGNFAPVPEHAADGLPVVGK
IPKCIDGVYVRNGANFLYEPVACHHFFDGDGMVHAVKFTNGAASYACRFTETQRLSQE
KSLGRPVFPKAIGELHGHSGIARLLLFYARGLFGLVDGSQGMGVANAGLVYFNNHLLA
MSEDDLPYHVRITPNGDITTVGKYDFNQCLUSTMIAHPKLDPVDGDLHALSYDVIORP
YLKYERESPDGVKSDDVEIPLKEPTMHIDFAITENFVVVPDQQVYFKLTENITGGSPV
VYDKNKTSRFGILHKNAKDANAMRWIDAPDCFCFHLWNAWEEPETEEVVVIGSCMTPA
DSIFNECEESLKSVLSBIRLNLRTGKSTRRFIISDAEQVNLEAGMVNRKLGRKTQFA
VLALAEPWRKVSGFAKVDLLSGEVKYMYGEEKFGGEPLFLPNGQKEDDGYILAFVHD
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/product="neoxanthin cleavage
/protein_id="nah811932.1"
/db_xref="GI:9857290"
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The 9-cis-epoxycarotenoid cleavage reaction is the key step of abscisic acid biosynthesis in water-stressed be proc. Natl. Acad. Sci. U.S.A. 96 (26), 15354-15361 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aagttaagaaacatctttacggcgataaccgttacggaggagagcctctgtttctccccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCTGGCCGAGCCCTGGCCCAAAGTCTCGGGCTTTGCGAAAGTTGATTTGTTCAGTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCATTTTCAATGAATGCGATGAGAGTTTGAAGAGCGTCTTGTCTGAGATAAGGCTGAACT
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            Direct Submission
Submitted (15-JUL-2000) The I
Medical Center Dr, Rockville,
                                                                                                l (bases 1 to 72058)
Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fras Arabidopsis thaliana chromosome 1 BAC T2H7 genomic sequence
                                                     2 (bases 1 to 72058)
Town, C.D. and Kaul, S.
                                                                                     Unpublished
                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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genomic
               cdtown@tigr.org
                            Research,
                                                                                                                              Utterback, T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission Submitted (19-JAN-2001) The Institute for Genomic Research, 9 Submitted (19-JAN-2001) The Institute for Genomic Research, 9 Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org On Jan 19, 2001 this sequence version replaced gi:12280878. Address all correspondence to:at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prediction programs including Genscan+ (Chris Burge,
http://CCR-081.mit.edu/GENSCAN.html), GenemarkHMM (Mark Borodovsky,
http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant
of GlimmerM, see Mihaela Pertea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 (bases 1 to 72058)
Town, C.D. and Kaul, S.
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                                                                                                                                                                 complement(3313. .3366)
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complement(4636. .4686)
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                                                                  complement(4636...4686)
/rpt_family="AT_rich"
complement(5249...5270)
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2828.
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                                    complement(<7213. .>8049)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQGVLCMNREQLEELRVTPLSASSASKRTLVPALNMRLWYAPELDLPDGTVLKGATLV
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(Arabidopsis thaliana)"
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/chromosome="I"
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/cultivar="Columbia"
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                                                                                                                                                                                                                                                                                _family="(GAAAA)n"
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complement(13002...16330)
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complement(7213.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family "ATCOPIA121 ATCOPIA12I Internal region ATCOPIA12 LTR-retrotransposon." complement(14311. 14498) /rpt_family "ATCOPIA13I ATCOPIA13I Internal region ATCOPIA13 LTR-retrotransposon." complement(15657. .16345)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(14226. 14687)
/rpt_family="ATCOPIA221|ATCOPIA221 -
sequence."
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/rpt_family="Arcopia141|Arcopia141 Internal region of
Arcopia14 Lfr-retrotransposon."
complement(14032 .14866)
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complement(11013. .110)
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complement(10873...10
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/rpt_family="AT_rich"
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PIPVLTYRENTKDGEIKNPKDVEFRNPEEEDEPMVKDIICVSPPEKIVRVVSEKKQRD
DVAMEEYKPVTEQTLASEEACNTRNHVNPNKPYGRSKSDKPRRKRLSVDTETTKRKSY
                                                                                                                                                                                                                                              complement(17528. .17576)
                                                                                                                                                                                                                                                                        FMVFREEETTEERFMCYTDDIGDLCIFVSKSEAFCVPASSYPGLKPNSIYFVGFGLG: YDLTTRNVSIFRAPKGALNQIVSPYWFPPASS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="T2H7.3"
/note="predicted by genemark hmm"
join(17486. .17518,17796. .18535,18620. .18947)
/gene="T2H7.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(14308. .14492)
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/protein_id="AAG50854,1"
/db_xref="G1:12321638"
/translation="MTEMPSYMIENPKFEPKKRRYYSSSMLTIFLPIFTYIMIFHVFE
                                                                                                   complement(19380. .20533)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
/protein_id="AAG50857.1"
/db_xref="GI:12321631"
/note="similar to hypothetical protein GI:8778720 from
(Arabidopsis thaliana)"
                                                                                                                                                                                                                                                                                                                                                     {	t RNFPESLKYDSELSELFPSSCRTERFVESPSGDERFLVKWYAKGCLASSSKITYETQR}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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TTCGGTTTATTAAATCACAAAAACGGAACCGGAGTTGCTAACGCCGGTTTGGTTTACTTC
                                                            GGTGAGCTACATGGTCACTCTGGAATCGCACGGTTGATGCTATTTTACGCACGTGGTTTA
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/gene="T2H7.5"
/gene="TiH7.5"
/note="similar to En Spm like transposon protein
GI:4115361 from (Arabidopsis thaliana)"
complement()oin(21856. .2230,22534. .22806,2304:
23290. .23520,24442. .24837))
/gene="T2H7.5"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="En/Spm-like transposon protein, putative" /protein_id="AAG50859.1" /protein_id="AAG50859.1" /db_xref="GI:12321633" /translation="MSSSSAIKAAAKALERIRIMDTVRSSYVGLFSSTVTDMVSKNRF /KRGQCIVLQIARGVARALNIPEDAVEVKTLHNSWTCYEIVHTVKTPMAAPPKRGMPTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(21745..21765)
/rpt_family="AT_rich"
complement(join(<21856...</pre>
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/gene="T2H7.4"
/codon_start=1
/product="unknown protein"
/protein_id="AAG50858.1"
/db_xref="GI:13321633"
/db_xref="GI:13321633"
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23290...23520,24442...>24837))
/gene="T2H7.5"
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/rpt_family="AT_rich"
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PYASKSKPKMIHLPFFTPMYSGQTEVVCNVAMSSPPPDQDDDHEDWVVGIKFLGRQLS
LCRPRHDLRWTNILTPFESWEVSELMYSKKDQRFYLLAPGGNYLCSWDLNFKEDKKPK
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IVMVFREEETKDGKKNMRYTDDIGDLCIFISKGEDFCVKASSCPGLQPNSISLHGRLF
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68.2%;
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              GAAAAACGATTGGGTCGACCAGTTTTCCCGAAAGCAATCGGCGAGCTTCACGGTCACTCG
                                                     GAAGGAACAATCCCTGACTGCATTGACGGTGTTTATATCCGTAACGGCGCGAATCCGATG
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Eukaryota; Viridiplantae; Streptoph
Spermatophyta; Magnoliophyta; eudic
Rosidae; eurosids II; Brassicales;
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Patent: EP 1116794-A 1 18-JUL-2001;
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//db_xref="01:14347190"
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Submitted (03-FEB-1998) MIPS, at the Max-Planck-Institut fuer Submitted (03-FEB-1998) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="strong similarity to neoxanthin cleavage enzyme, Lycopersicon esculentum, PATCHX:E325797; and viviparous-14, Zea mays, PATCHX:G2232017"
contains
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                                                          note="strong similarity to (S)-2-hydroxy-acid oxidase
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                                       .3.15), peroxisomal,
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                                       Spinacia
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e 4, BAC clone F28J12 (ESSAII
                                         oleracea (spinach)
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/gene="F28J12.20"
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complement(5646.
                                                                                                                  complement(7235./gene="F28J12.20
                                                                                                                                                                                                   complement(7188.
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/number=¤
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EGRIPVFLDGGVRRGTDVFKALALGASGVFVGRPSLFSLAADGEAGVRKMLQMLRDEF
ELTMALSGCRSLREISRTHIKTDWDTPHYLSAKL"
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Query Match 41.0
Best Local Similarity 68.2
Matches 1063; Conservative
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9450. .9577
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8913. .90
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PATCHX:G1184684
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join(8557. .8838,
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/gene="F28J12.30"
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. .10368,12117. .12725,12806. .13321,13362. .13622,
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Pred. No. 3.2e-208;
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Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: Lencke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
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Murphy,G., Ridley,P.,
Mayer,K.F.X.
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Hilbert, H., Braun, M., Holzer, E., Brandt, A., Duesterhoeft, A., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.
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EEIKTLPLNGDRVKLQLILADLLRNIVNHAPFPNSWVGISISPGQELSRDNGRYIHLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPLIPPIFASDENACCSEWNAAMEKLTGWSKHEVIGKMLPGEVFGVFCKVKCQDSLTK
FLISLYQGIAGDNVPESSLVEFFNKEGKYIEASLTANKSTNIEGKVIRCFFFLQIINK
ESGLSCPELKESAQSLNELTYVRQEIKNPLNGIRFAHKLLESSEISASQRQFLETSDA
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GALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDLEPYLGLHYPATDIPQA
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complement(15338.
                                                                                                                                                                                                                                                                               QRFYRDSCILSDGIYTKDLTVLGLDLAKVAIVDNCPQVYRLQINNGIPIKSWYDDPTD
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1144 aaggtcgcaagattcgggattttagacaaatacgccgaagattcatcgaacattaagtgg 1203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cagatcgccggaaattttgctccggtgaatgaacagcccgtccggcgtaatcttccggtg 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ggtttccttgtcagccacgagaagctacacccgcttcctaaaacggctgatcctagtgtt 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATCCTCTCCGGCTAAACATCTTCCAGAAAGCGGCGGCGATTGCGATCGACGCGGCTGAG 110204
                                                                                                                                                                                                                        tacttccgattctcaccggacggaactaaatcaccggacgtcgagattcagcttgatcag 1023
                                                                                                                                                                                                                                                                                                                                                           GGACGTTACGATTTCGACGGTCAGTTAAAATCCGCAATGATAGCTCACCCGAAACTGGAC 110804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cacggaaccggtgtagctaacgccggtttggtctatttcaatggccggttattggctatg 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAAAACGATTGGGTCGACCAGTTTTCCCGAAAGCAATCGGCGAGCTTCACGGTCACTCG 110564
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                                                               gtcgttttcaagctgccggagatgatccgcggtgggtctccggtggttttacgacaagaac 1143
                                                                                                                                       ccaacgatgatgcacgatttcgcgattacagagaacttcgtcgtcgtcctgacctgaccagcaa 1083
                                                                                                                                                                                                                                                                               CCGGTTACGAAGGAGCTTCACGCGTTAAGCTACGACGTCGTTAAGAAAACCTTACCTGAAA 110864
                                                                                                                                                                                                                                                                                                  coggaatcoggtgaactcttogctttaagctacgacgtcgtttcaaagccttacctaaaa 963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACGGCGTCGGAGTAGCAAACGCCGGTTTGGTTTACTTTAATAACCGGCTTTTAGCTATG
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                                         GTCGTGTTCAAGCTCGGCGAGATGATTTCCGGTAAATCTCCGGTTGTTTTCGACGGAGAA 111044
                                                                                                                     CCGACGATGATTCACGATTTCGCTATAACGGAGAATTTTGTGGTGATTCCTGATCAACAA 110984
                                                                                                                                                                                                   TACTTCAGATTCTCGCCAGACGGCGTTAAATCGCCGGAATTGGAGATCCCGCTCGAAACT 110924
                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAGAAGACGATTTACCGTACCAATTAAAAATTACTCAAACCGGCGATCTCCAAACCGTT
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68.2%;
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Pred. No. 3.6e-208;
0; Mismatches 478;
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망 Š 밁 ρ В В δÃ В Ş В Ş В Š 뫄 δÃ В δõ В δõ Ş 111285 111045 AAGGTTTCCCGATTGGGGATAATGCCCAAGGACGCGACAGAAGCTTCTCAGATAATCTGG 111639 111579 111519 111459 111399 111339 111165 111105 1324 1612 1564 tacggcgataaccgttacggaggagagcctctgtttctccccgg------agaa 1611 1504 1444 1384 1204 attgatgetecagattgettetgettecatetetgggaacgettgggaagagecagaaaca 1263 aacagaaacatgctcggccgtaaaaccaaattcgcttacttggctttagccgagccgtgg 1503 actcgccgtccgatcatctccaacgaagatcaaccaagtcaacctcgaagcagggatggtc 1443 GAAGAAAATGAAGATGACGGTTATATATTTTGTCACGTTCATGACGAAGAACAAAGACA 111578 ggaggagaggaggaagacgaaggatacatcctctgtttcgttcacgacgagaagacatggaaa 1671 TACGGCGGTGAGAAATATGGCGGCGAACCGTTTTTCTTGCCCGGCAACTCCGGTAACGGC 111518 CCAAAAGTTTCCGGTTTCGCTAAGGTCGATCTTTGCACCGGTGAGATGAAAAAAATATATT 111458 cctaaagtctcaggattcgctaaagttgatctcactactggagaagttaagaaacatctt 1563 ACGCGTCGTTCGTTGCTTAACGAGGAT------GTAAATTTAGAGATTGGTATGGTT 111338 GTGAACTCTCCGGAGACGTTCTGTTTTCATCTCTGGAATGCATGGGAATCGCCGGAGACG 111164 111638 111398 111104

Search completed: July 24, 2002, 07:42:25 Job time: 7835 sec

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Copyright (c) 1993 - 2000 Compugen Ltd
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Arabidopsis thalia
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ALIGNMENTS

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                           13-JAN-2000; 2000JP-0010056
11-JAN-2001; 2001JP-0003476
                                                                                                                                                                                                Neoxanthin cleavage enzyme: AtNCED3; abscisic acid; ABA; herbicide; stress tolerance; transgenic plant; plant breeding; antisense-therapy;
                                                                                                                                                                                                                                                   10-SEP-2001
                                                                                                                                                                                                                                                                      AAD09396;
                                                                                                                                                                                                                                                                                          AAD09396 standard; cDNA; 1800
        (RIKE ) RIKEN KK
                                                        11-JAN-2001; 2001EP-0300218
                                                                            18-JUL-2001.
                                                                                                EP1116794-A2
                                                                                                                                                                    Arabidopsis thaliana.
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                                                                                                                                      Location/Qualifiers
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/product= "Arabidopsis thaliana AtNCED3 protein"
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AAC56695

Eucalyptus

grandis

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The invention relates to neoxanthin cleavage enzymes and their corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key corle in endogenous abscisic acid (ABA) biosynthesis under drought stress. Reoxanthin cleavage enzyme is used for improving stress tolerance in a plant when expressed in a plant cell. The invention also relates to methods for increasing or decreasing stress tolerance in a plant by comethods for increasing or decreasing stress tolerance in a plant by comethods for increasing or decreasing stress tolerance in a plant by comeoxanthin cleavage enzyme is introduced. The improvement of stress coneoxanthin cleavage enzyme genes are useful for producing transgenic plants. An arid land can be improved by growing transformant weed for several years and contained the removing the weed by specifically lowering stress tolerance in the weed by inducing an inducible promoter. The present cDNA sequence encodes arabidopsis thaliana neoxanthin cleavage enzyme, AtNCED3 protein.

The AtNCED3 cDNA is obtained from an Arabidopsis plant-derived cDNA companies in the companies of the CPRD65 (CowPea Responsive to Dehydration) gene isolated from cowpea plant as a probe.
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Best Local Similarity 100.0%;
Matches 1800; Conservative 0
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             The invention relates to neoxanthin cleavage enzymes and their corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key role in endogenous abscisic acid (ABA) biosynthesis under drought stress. Neoxanthin cleavage enzyme is used for improving stress tolerance in a plant when expressed in a plant cell. The invention also relates to methods for increasing or decreasing stress tolerance in a plant by introducing the DNA into the plant, and a transgenic plant into which a neoxanthin cleavage enzyme is introduced. The improvement of stress tolerance in plants is useful, for example in plant breeding. Neoxanthin cleavage enzyme genes are useful for producing transgenic plants. An arid land can be improved by growing transformant weed for several years and then removing the weed by growing transformant weed for several years and then removing an inducible promoter. The present cDNA sequence encodes by copersicon esculentum neoxanthin cleavage enzyme, LeNCED1 protein
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11-JAN-2001;
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2001JP-0003476
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                                                                                                                                                                                                                                                                                                                              corresponding CDNA molecules. Neoxanthin cleavage enzyme plays a key role in endogenous abscisic acid (ABA) biosynthesis under drought stress. Neoxanthin cleavage enzyme is used for improving stress tolerance in a plant when expressed in a plant cell. The invention also relates to methods for increasing or decreasing stress tolerance in a plant by introducing the DNA into the plant, and a transgenic plant into which a neoxanthin cleavage enzyme is introduced. The improvement of stress tolerance in plants is useful, for example in plant breeding. Neoxanthin cleavage enzyme genes are useful for producing transgenic plants. An arid land can be improved by growing transformant weed for several years and then removing the weed by specifically lowering stress tolerance in the weed by inducing an inducible promoter. The present cDNA sequence encodes vigna unguiculata neoxanthin cleavage enzyme, CPRD65 (CowPea Responsive to Dehydration) protein. CPRD65 gene is isolated from cowpea plant.
                                                                                                                  Query Match
Best Local
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Best Local
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The invention relates to neoxanthin cleavage enzymes and their corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key role in endogenous abscisic acid (ABA) biosynthesis under drought stress. Neoxanthin cleavage enzyme is used for improving stress tolerance in a plant when expressed in a plant cell. The invention also relates to methods for increasing or decreasing stress tolerance in a plant by

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11-JAN-2001;
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transgenic plant; plant breeding; antisense-therapy;
ectant; ss.
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neoxanthin cleavage enzyme is introduced. The improvement of stress tolerance in plants is useful, for example in plant breeding. Neoxanthin cleavage enzyme genes are useful for producing transgenic plants. An arid land can be improved by growing transformant weed for several years and then removing the weed by specifically lowering stress tolerance in the weed by inducing an inducible promoter. The present cDNA sequence encodes seem anys neoxanthin cleavage enzyme, VP14 protein related to the
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10-SEP-2001 (first entry)

Arabidopsis thaliana neoxanthin cleavage enzyme, AtNCED5 cDNA

Neoxanthin cleavage enzyme; AtNCED5; stress tolerance; transgenic plant; p plant breeding; acid; ABA; herbicide; antisense-therapy;

growth protectant; SS

Location/Qualifiers
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/product= /*tag= "Arabidopsis thaliana AtNCED5 protein"

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Best Loc
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                                                                                  <u>ggagtttgtggtggtcgacgcgacggatatgaagcaagtcgcggcggtgcgcttgccgga</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may
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18-AUG-1999;
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                     This invention describes a novel polynucleotide sequence (I) which encodes a protein capable of regulating the synthesis of abscisic acid. The invention also describes (1) an oligonucleotide encoding a protein of a gene obtained by controlling the expression of a VP14-like gene; (2) a vector containing the oligonucleotide ligated operably to the regulation sequence; (3) a plant transformed with the vector; and (4) a method for regulating abscisic acid synthesis in a plant including the transfer of the above oligonucleotide to it. The gene is useful for constructing drought resistant rice.
                                                                                                                                                                                                  Oligonucleotide encoding gene for regulating abscisic acid synthesis plants, useful for constructing e.g. genetically-modified rice with drought resistance and ear-germination resistance \dot{\ }
                                                                                                                                                                                                                                                                                                                    (NORQ )
(BIOO-)
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BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT
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                                                                                                                                                                                                                                                                                         Sakamoto
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Sequence

492 BP;

90 A;

126 C;

186 G; 88 Η. N other;

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Best Local (
                                                                                                                                                                                                                     Plant; transcription factor; gene expression; eucalyptus; pine; poplar; sweetgum; teak; mahogany; b&IF; G-box binding factor; basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain; type 2 Cys2His2; CCAAT box element; MYB; ss.
                                                                                         11-MAR-1999;
18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                1046
                                 Wood M,
                                                                                                                             09-MAR-2000;
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                                                                                                                                                                                                 Eucalyptus grandis
                                                                                                                                                                                                                                                                                           Eucalyptus grandis transcription factor DNA sequence #566
                                                                                                                                                                                                                                                                                                                                                                 AAC56695
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                                                       GENESIS R
FLETCHER
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                                                                                                                                                                                                                                                                                                                                                                 standard;
                               McGrath A,
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                                                                                                                             2000WO-US06112
                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                          99US-0266513
99US-0149485
                                                       RES & DEV CORP LTD.
R CHALLENGE FORESTS
                                                                                                                                                                                                                                                                                                                                                                 DNA;
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69.7%;
                                 Shenk
                                 MΑ,
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Pred. No. 2
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                                                        LTD.
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.1e-55;
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New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
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Claim ۲, Page 494; 747pp; English

Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acada, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic helix-loop-helix zipper, LIM domain, AP2 and EREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements The present invention relates to novel plant transcription factors from

Sequence 372 B₽; 60 A; 148 C; 101 <u>ი</u> 63 Τ; 0

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Query Match
Best Local Similarity
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361
                        999
                                                   301
                                                                                                     241
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             ggacgtcgagat 1010
                                                             gatgatcgcccacccgaagatcgacccggcttccggcgagatgttcgccctcagctacga
                                                                                                                 aatgattgcccacccgaaagtcgacccggaatccggtgaactcttcgctttaagctacga
                                                                                                                                                                     tcccaatggagatttaaaaaaccgttggtcggttcgattttgatggacaattagaatccac
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                                                                                                                                                                                                                                                                          tgcagccggtatagtcgacccggcacacggaaccggtgtagctaacgccggttttggtcta
                                                 cgtcgtccggaagccgtacctcaagtacttccgattctccaaggacggcgagaagtcccc
                                                                                                                                                      gcgctccggcgacctcgagaccgtcggccgctacgacttcgccggccagctcgactctcc
                                                                                                                                                                                                          cttcgacggccacctcctcgcgatgtccgaggacgacctcccctaccacgtgcgcgtcac
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372
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Pred.
                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                              188;
No. 2.
                                                                                                                                                                                                                                                                                                                                                                              DB 21;
.8e-50;
                                                                                                                                                                                                                                                                                                                                                                    115;
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DЬ

Qy DЬ

Qγ DЪ δÃ

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AAC56548 standard; DNA; ΒP

25-JAN-2001 (first entry)

Eucalyptus grandis transcription factor DNA sequence #419

RESULT 10
AAC56548
ID AAC565
XX AAC565
XX AC565
XX DT 25-JAN
XX Eucaly
XX Plant;
KW poplar
KW basic
KW basic
KW homeod
KW type 2
XX
OS Eucaly poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain; type 2 Cys2His2; CCAAT box element; MYB: se MADS;

Eucalyptus grandis

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RESULT 1
AAC42989
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Best Local S
Matches 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAR-1999;
18-AUG-1999;
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                           AAC42989 standard; DNA; 1788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 9.5%;
Local Similarity 71.2%;
nes 227; Conservative
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                                                    The invention relates to neoxanthin cleavage enzymes and their corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key crole in endogenous abscisic acid (ABA) biosynthesis under drought stress. Neoxanthin cleavage enzyme is used for improving stress tolerance in a plant when expressed in a plant cell. The invention also relates to methods for increasing or decreasing stress tolerance in a plant by the DNA into the plant, and a transgenic plant into which a neoxanthin cleavage enzyme is introduced. The improvement of stress tolerance in plants is useful, for example in plant breeding. Neoxanthin cleavage enzyme genes are useful for producing transgenic plants. An arid cleavage enzyme genes are useful for producing transgenic plants and then removing the weed by growing transformant weed for several years and then removing the weed by specifically lowering stress tolerance in the weed by inducing an inducible promoter. The present cDNA sequence encodes Arabidopsis thaliana neoxanthin cleavage enzyme, AtNCED2 protein.
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      Claim
                                                      Novel isolated defence-related signalling gene isolated from encoding neoxanthin cleavage enzyme, amino acid permease or gacid-rich protein useful for increasing resistance of plant toathogen
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P-PSDB; AAB72303.
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23-MAY-2000;
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                                                                                                                                                                                                                                                                (PION-) PIONEER HI-BRED (CURA-) CURAGEN CORP.
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Pred. No. 9.2e-44;
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Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic helix-loop-helix zipper, LIM domain, AP2 and EREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements

present invention

relates to novel

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18-AUG-1999;
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2000-579369/54
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                                          GENESIS R
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                                                                                                              2000WO-US06112
                                                                           99US-0266513.
99US-0149485.
                                                      RES & DEV CORP
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                                                                                                                                                                                                       CCAAT box element; MYB; ss
                                           CHALLENGE FORESTS
                                                                                                                                                                                                                                                                                                                                           DNA;
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New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
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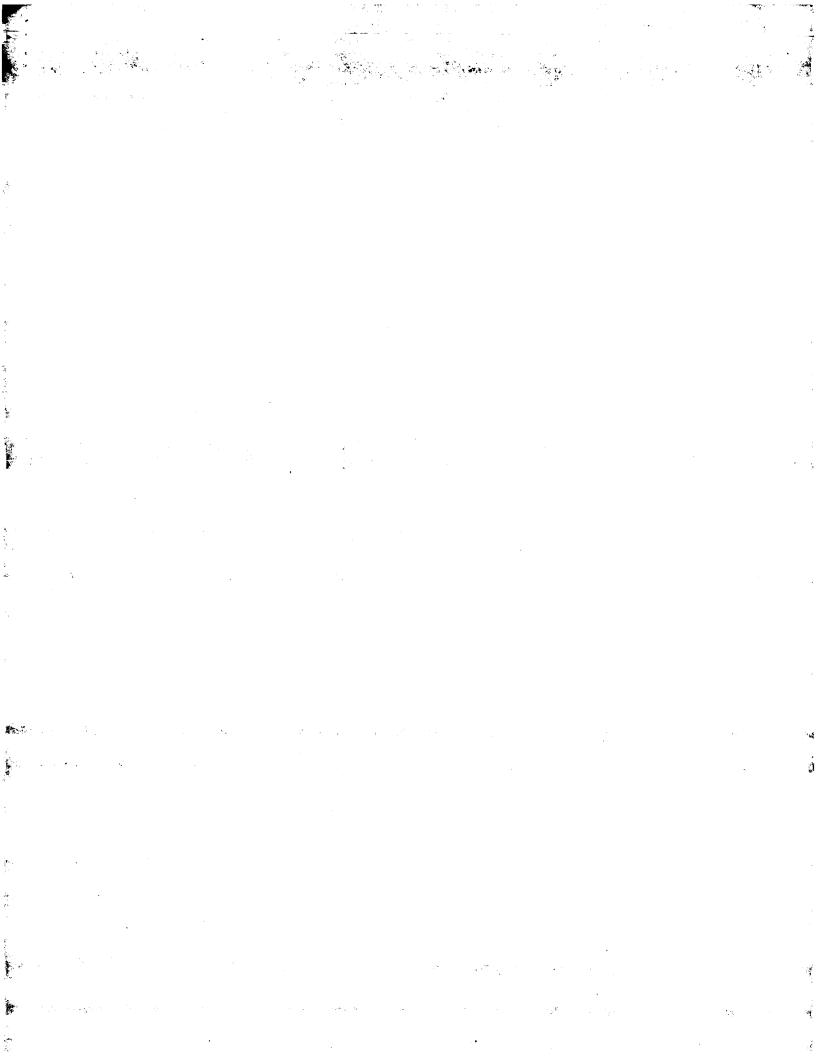
Claim 1; Page 599; 747pp; English.

The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor mabe used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic helix-loop-helix zipper, homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2 and ERBBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements may

Sequence 386 BP; 89 Α, 105 ü 106 G; 86 Τ; 0 other;

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Search co completed: ne: 6890 sec July 24,



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Copyright (c) 1993 - 2000 Compugen
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AW933524 EST359283
BM408565 EST482892
BF113346 EST440936
BE461924 EST413439
BM085672 saj32802.
BM085672 saj32802.
BM085075 saj31408.
BE432853 EST399478
BH4559796 BOHRRA7TF
BH458011 BOHBT02TF
BH974879 sai74bi1.
BE437072 EST408190
BE43861 EST408190
BE43861 EST414153
BM084948 saj30b08.
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BM408615 EST582942
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ALIGNMENTS

ACCESSION VERSION KEYWORDS RESULT 1
BM412731
LOCUS
DEFINITION COMMENT FEATURES REFERENCE SOURCE TITLE JOURNAL AUTHORS ORGANISM source 1 (bases 1 to 720)
Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Ts.,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue, breaker stage (2002) Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum; BM412731 720 bp mRNA linear EST 22-JAN-200 EST587047 tomato breaker fruit Lycopersicon esculentum cDNA clone cLEG60N24 5' end, mRNA sequence.
BM412731 BM412731.1 GI:18264350 EST. Clemson University 100 Jordan Hall, Clemson, Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics Contact: CUGI Clemson University Genomics Institute Unpublished (2002) Seq primer: T3 tomato. Lycopersicon. /clone_lib="tomato breaker /tissue_type="Pericarp" /dev_stage="breaker" /organism="Lycopersicon /cultivar="TA496" /db_xref="taxon:4081" /clone="cleg60N24" /note="Vector: pBluescriptSKmCUadapt; Site_1:
Site_2: XhoI; supplier: Boyce Thompson Institu /lab_host="SOLR" Location/Qualifiers SC 29634, USA esculentum" EST 22-JAN-2002

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EST582942 tc
CLEG45023 5'
BM408615
BM408615.1
  Lycopersicon esculentum 
Eukaryota; Viridiplantae;
                            tomato.
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                                                                           tomato
5' end,
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breaker fruit 1
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No. 6.
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Lycopersicon
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5.3e-116;
 Embryophyta;
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Clemson University Genomics
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Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue, breaker stage (200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: http://www.genome.clemson.edu/orders, This clone is available through the Clemson
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/tissue_type="Pericarp"
/dev_stage="breaker"
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Tel: 301-838-3523
Fax: 301-838-0208
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Whole genome shotgun sequencing of Brassica
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Alcala,J., Vrebalov,J., White,R., Matern,A.L.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L.,
Fraser,C.M., Martin,G.B., Tanksley,S.D. and G
Generation of ESTs from tomato fruit tissue
                                                                                Lycopersicon esculentum

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On May 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
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a 130 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seeds and locules were discarded prior to freezing the
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/clone="cLEF54E2"
/clone_ib="tomato fruit mature green,
/tissue_type="fruit pericarp"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="SOLR"
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                      ccggtgaatgaacagcccgtccggcgtaatcttccggttggtcggaaaacttcccgattcc
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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BM408565.1 GI:18260195
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a 194 c 165 g 212 t
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/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
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/cultivar="TA496"
/db_xref="taxon:4081"
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                                                                                                                                                     Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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Alcala,J., Vrebalov,J.,
Llang,F., Hansen,T.S.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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/clone="cLEG44B9"
/clone_lib="tomato breaker
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
                                                                                           /organism="Lycopersicon
/cultivar="TA496"
                                                                              /db_xref="taxon:4081"
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Craven,M.B., Bowman,C.L., Ronning,C.M.,
L., Martin,G.B., Giovannoni,J.J. and Tanksley
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                                             Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo.
Eukaryota; Wagnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Solanales; Solanaceae; Solanum;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
              Alcala, J.,
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                Vrebalov,J.,
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                Holt, I.E.,
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Liang, F.,

Hansen, T.S.,

Bowman, C.L.,

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/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
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/clone="cLEG40L2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BM085672 553 bp mRNA linear EST 19-NOV-20 saj28a02.y1 Gm-c1066 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1066-3867.5' similar to TR:024023 024023 NEOXANTHIN CLEAVAGE
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BM085672
BM085672.1 GI:16996300
EST.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Shoemaker R/Public Soybean
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Public Soybean EST Project
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ilarity 74.1%;
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                                                                                                                                                                                           /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from unexpanded leaves and the shoot tips of 2 week old seedling from the cultivar Williams. The 2 week old seedlings were salt stressed in a solution of 500mM Nacl for 3 days prior to harvesting. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               est@watson.wustl.edu
                                                                                                                                                      Ø
                                                                                                                                                                              Shoemaker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Leaf and shoot tip, salt stressed, 2 week
old seedling"
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/db_xref="taxon:3847"
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/clone_lib="Gm-c1066"
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                 This clone is available through: ResGen, Invitrogen Corp. South Memorial Parkway Huntsville, AL 35801 For further in call: (800)-533-4363 or contact: ccu@resgen.com web site: www.resgen.com
                                                                                        Contact: Shoemaker R/Public Soybean EST F
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1810
Fax: 314 286 1810
Email: estéwatson.wustl.edu
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old seedling"
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GTTTACGACAAGAACAAAGTTTCCCGATTTGGTATTCTGGATAAGTACGCGAAAGATGGG
                                                                   ATTCCTGATCAACAAGTCGTTTTCAAGATGTCTGAAATGATCCGTGGAGGTTCACCGGTG
                                                                                                                                       ATTCCAGTTGAAGACCCAACAATGATGCATGATTTCGCAATTACTGAGAACTTCGTCGTC
                                                                                                                                                                                                          AAGCCATACCTCAAGTACTTCAGATTTTCAAAAAATGGGGGAAAAATCAAATGATGTTGAA
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Clemson University
100 Jordan Hall, Clemson, SC 29634, U
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
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EST399478 tomato
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http://www.genome.clemson.edu/orders/index.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBluescriptSKmcUadapt; Site_1: EcoR1; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

100 c 116 g 148 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Lycopersicon esc
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEG11G7"
/clone_lib="tomato breaker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
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75.9%;
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to breaker fruit,
mRNA sequence.
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Pred. No. 2.2e-83;
0; Mismatches 124;
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Lycopersicon esculentum cDNA
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AUTHORS
TITLE
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SOURCE
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Best Local S
Matches 354
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                                                                                                                                               catttccctaagcaatcatcaaactctccccgccattgttgttaagcccaaagccaaagcaaagaa
                                                           gccagtcgtgtcacacgtaagctcaatgtttcatctgcgcttcacactcctcccagctctt 180
                                                                                                 AAACCACCATTATCGTCTTCTCAAAAGCTCCGCCTTGGGTTATTCTTGCTCCGTACCCATG 440
                                                                                                              cagccgccattatcgtcttctcaaagctccgacttgagttattgtagctccttacctatg 120
CATTTCCCCAAGCAATCCTCCACCTCTCCCGCCATTGTTGTGAACCCCAAAACCAAAGAA
                                              ACAAATCGTTCCCAACGAAAGCTCAATGTTTCTTCTGCGCTTCACACTCATCCTGCTCTC 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence.
BH559796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whole genome shotgun sequencing Unpublished (2001) Other_GSSs: BOHRR47TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

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1 (bases 1 to 742)
1 Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Drive, Tel: 301-838-3523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Chris Town
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                                                                                                                                                                                                                                                                                                                                                                                                                         DNA is from
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                                                                                                                                                                                                                                                                                                                                                                                                              primer:
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                                                                                                                                                                                                                                                                                                                                                                                                                         cdtown@tigr.org
from a doubled |
                                                                                                                                                                                                                                                                                                                       /organism="Brassica ole
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHRR47"
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                                                                                                                                                                                                                                                                         genomic
a 235
                                                                                                                                                                                                                                                                        /clone_lib="BOHR"
/note="Vector: pHOS1; Site_1: BstXI; /genomic DNA inserted into pHOS1 using 235 c 117 g 200 t
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1. .742
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84.1%;
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                                agacaaatacgccgaagattcatcgaacattaagtggattgatgctccagattgcttctg 1226
                                                                                                                                            gattacagagaacttcgtcgtcgtacctgaccagcaagtcgttttcaagctgccggagat 1106
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GAGCAAATACGCTGAAGACGCTTCGTCGATGCGGTGGATCGAGGTGGAAGACTGCTTCTG
                                                                                                                                                                                                                           GATCACGGAGAACTTCGTCGTGGTTCCGACCCAGCAAGTGGTGTTCAGGCTACCGGAGAT 535
                                                                                                               GATCCGCGGCGGCTCTCCGGTGGTTTACGACAAAAACAAGAAATCAAGATTCGGTGTTTT 475
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TIGR
9712 Medical Center |
Tel: 301-838-3523
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Other_GSSs: BOHBTO2TR
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Brassica oleracea
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Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
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/strain="TOL000DH3"
/db_xref="taxon:3712"
/clone="BOHBT02"
/clone=1bb="BOHBT02"
/clone=1bb="BOHB"
/clone=1bb
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                                                                                                                Possible reversed clone: similarity on wrong strand This available through: ResGen, Invitrogen Corp. 2130 South Me Parkway Huntsville, AL 35801 For further information call )-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 423.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
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                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                    Public Soybean EST Project
Washington University School of Medicine
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Ritter, E., Kohn, S., Shin, T.,
Waterston, R. and Wilson, R.
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c!/
/clone_lib="Gm-c1068"
/tissue_type="Leaf, drought stressed,
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         EST408190 tomato breaker fruit, clone cLEG35K8, mRNA sequence.
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/lab_host="DH10B"
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  TCGATTTCGACGGCCAGCTAAAATCCACCATGATAGCTCACCCAAAGCTCGACCCAGTTT
                   tcgattttgatggacaattagaatccacaatgattgcccacccgaaagtcgacccggaat 910
                                                                                   ATGATTTGCCTTACCATGTAAAGGTAACACCCACCGGCGATCTTAAAACAGAGGGTCGAT
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5 prime
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Contact: CUGI
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Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Egukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                locules were discarded prior to freezing the pericarp. 133\ c 120\ g 154\ t
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/clone_lib="tomato breaker
/tissue_type="Pericarp"
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/lab_host="SOLR"
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ggaaaacttcccgattccatcaaaggagtgtatgtgcgcaacggagctaacccacttcac
                                     ATTTCTGGGAATTTTGCTCCGGTACCGGAAAATCCAGTCTGTCAATCTCTTCCGGTCACC
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EST414153 tomato developing/immature green fruit Lycopersicon esculentum cDNA clone cLEM4F10, mRNA sequence.
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Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksle
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Clemson University
100 Jordan Hall, Clemson, SC 29634, U
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Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicottyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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BE458861.1 GI:9503163
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18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prime sequence
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                                                                                                                                                                                                                                                                                                                                                           /note-"Vector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: Xhol; Fruit were tagged at 5 dpa (0.5 cm) and harvested at 7 day intervals through 35 dpa. Equal masses of tissue from each stage were combined (including seeds and locules) prior to mRNA isolation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="fruit"
/dev_stage="immature green (5-35
/lab_host="SOLR"
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/cultivar="TA496"
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/clone="cLEM4F10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="tomato developing/immature green fruit"
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Pred. No. 2.2e-79;
0; Mismatches 191
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                              GAAGATGATTTGCCTTACCATGTAAAGGTAACACCCACCGGCGATCTTAAAACAGAAGGT
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Search completed: July 24, 2002, 06:53:47 Job time: 5972 sec

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Result
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Perfect score:
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1: /cgn2_6/ptodata/1,

2: /ggn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,
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Match
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Listing first 45 summaries
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/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
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 US-08-232-463-14
5225348-3
US-08-434-881-1
US-08-977-771-1
US-09-361-773-1
US-09-026-408-12
US-09-026-408-12
US-09-062-451-177
US-08-991-789A-17
US-08-994-907-1
PCT-US96-10986-11
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US-08-494-907-2
PCT-US96-10986-2
US-08-494-907-2
PCT-US96-10986-3
US-08-494-907-3
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US-08-394-035C-4
US-09-385-982-558
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Patent No. 5225348
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CCATION US/0823246 ON: NER, F. EIFILINGER, F. KNER, F. G. ION: RECOMBINANT NCES: 52 ADDRESS: Oley & Lardner Diagonal Road, S dria 299 ELE FORM: Floppy disk M PC COmpatible TEM: PC-DOS/MS-D TENIT Release #1 TION DATA: UMBER: US/07/935 UMBER: US/07/935 UMBER: EP 91 114 26-AUG-1991 10-OKMATION: TON DATA: UMBER: 29,768 NIMMBER: 29,768 NIMBER: 29,768 NIMMBER: 29,768 NIMMBER: 29,768 NIMMBER: 29,768 NIMMBER: 29,768 N		
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FILING DATE: 08-DEC-1989
SEQ ID NO:3:
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; APPLICANT: HAGATA, SHIGEKAZU;SUGANO, SUMIO;KIM, DONG W.;
;UETSUKI, TAICHI;KAZIRO, YOSHITO
; TITLE OF INVENTION: DNA FRAGMENT AND EXPRESSION PLASMID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONTAINING THE DNA FRAGMENT
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
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Best Local Similarity
Matches 99; Conserv
                                                                                                                                                    Sequence 1, Application US/08434881 Patent No. 5804376
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                                                                                                                                    GENERAL INFORMATION:
                                     APPLICANT: Braxton, Scott M.
APPLICANT: Wilde, Craig G.
APPLICANT: Diep, Dinh
TITLE OF INVENTION: PANCIPEAS-Derived Serpin
NUMBER OF SEQUENCES: 2
CORRESPONDENCES: TOUTO DEBTE CONTRESS:
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                          ADDRESSEE:
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Palo Alto
            E: Incyte Pharmaceuticals, 3330 Hillview Avenue
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RESULT 4
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US-08-434-881-1
                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08977771 Patent No. 6013448
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
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LENGTH: 1221 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE PC-DOS/MS-DOS
COERRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                          APPLICANT: Wilde, CI
APPLICANT: Diep, Dir
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                             COUNTRY:
ZIP: 94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Luther, Barbara J
REGISTRATION NUMBER: 339
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: H
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                                                                                                                              CITY: Palo Alto
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                                                                                                            STATE:
                                                                                                                                           STREET:
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                                                                                                                                          E: Incyte Pharmaceuticals, 3330 Hillview Avenue
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                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                        Braxton,
   PatentIn Release #1.0,
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                                                                                                                                                                                                                                        Craig G.
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                PC-DOS/MS-DOS
                                                                                                                                                                                                            Pancreas-Derived Serpin
                                                                                                                                                                                                                                                      Scott M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Release #1.0, Version
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Pred. No. 0.51;
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   Version #1.30
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: CLASSIFICATION: FILING DATE:

08/ 434,881

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/977,771

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                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09361773
Patent No. 6197519
GENERAL INFORMATION:
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Best Local Similarity
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           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                     STREET: STREET: STREET: Palo Alto CITY: Palo Alto California
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NAME: Luther, Barbara J.
REGISTRATION NUMBER: 3399
                                                                                                                                                                                                                   APPLICANT: Diep, Dinh
TITLE OF INVENTION: Pancreas-Derived Serpin
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                APPLICANT: Braxton, Scott M.
APPLICANT: Wilde, Craig G.
APPLICANT: Diep, Dinh
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LOCATION:
                                                                                                          COUNTRY: UZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY:
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                                                                                                                                                                     E: Incyte Pharmaceuticals, Inc. 3330 Hillview Avenue
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US/09/361,773
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RESULT 6
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US-09-361-773-1
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Best Local Similarity
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ADDITCANT: Ni et al.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                       CLASSTET...

LIMPLY DISK

LIMPLY COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/026 *^^

FILING DATE: Herewit'

CLASSTET...
                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR TITLE OF INVENTION: INHIBITOR NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
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REGISTRATION NUMBER: 339
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                COUNTRY: USA
ZIP: 20005-3934
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1100 NEW YORK AVENUE, SUITE 600
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15-AUG-1997
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54.3%;
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Pred. No. 0.51;
0; Mismatches 58;
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US-09-026-408-1/c
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Best Local Similarity
Matches 69; Conserv
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                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY:
LOCATION:
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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LENGTH: 1370 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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LOCATION:
                                                                                                                                                                                                                                ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600 CITY: WASHINGTON
                                                APPLICATION NUMBER: UPFILING DATE: Herewith
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                                  CLASSIFICATION
                                                                                                                                                                                                 COUNTRY:
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APPLICATION DATA:
LICATION NUMBER:
                                                                                                                                                                                    20005-3934
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Conservative
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                                                                                                                                                                                                                                                                                                                   INHIBITOR
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                                                                 US/09/026,408
US 08/934,011
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Pred. No. 0.55;
0; Mismatches 58;
                                                                                                   #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58;
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US-08-991-789A-177
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                                                                                                                                                                                                                                                                                                                                                           Sequence 177, Application US/08991789A Patent No. 6225054
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 60/024,056
FILING DATE: 16-AUG-1996
ATTORREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600 TELEFAX: 202-371-2540
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1371 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97
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              SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,789A
                                                               ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                       APPLICAMAL - SMITH, John M.
Smith, John M.
Smith, John M.
Reed, Steven G.
Reed, Smith, John M.
Reed, Smith, John M.
Reed, Smith, John M.
Reed, Smith, John M.
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ADDRESSEE: Seed IP
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                                                                                                                                                                    CITY: Seattle
STATE: Washington
                                                                                                                                                                                                     STREET: 701 Fifth Avenue,
FILING DATE:
                                                                                                                                                       COUNTRY: USA
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109..1242
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67..1242
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67..108
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 11-Dec-1997
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Avenue, Suite 6300
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                                                   Version
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US-09-062-451-177
; Sequence 177, Application US/09062451
; Patent No. 6344550
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SEQUENCE CHARACTERISTICS:
LENCTH: 788 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local (
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GENERAL INFORMATION:
ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                   CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 1.9%;
Local Similarity 48.2%;
nes 94; Conservative
                                                                                                                CLASSIFICATION:
                                                                                                                                 APPLICATION NUMBER: FILING DATE: 04-AP
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                                                                                                                                                                                                                                                                                                  COUNTRY:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                               Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 210121.419C3
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                                                                                                                                                                                                                                                                                                                                                     6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                             Smith, John m.
Smith, John m.
Reed, Steven G.
Reed, Steven G.
ROUGHOSITIONS AND METHODS FOR THE
MORRATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Frudakis, Tony N.
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                                                                                                                                                                                                                                                                                                                                                                      SEED and BERRY LLP
                                                                                                                                 04-APR-1997
                                                                                                                                                   US/09/062,451
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                                      210121.419C2
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                                                        REFERENCE/DOCKET NUMBER: 0009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 559-6067
TELEFAX: (510) 559-5777
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1047 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
               MOLECULE TYPE:
                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Sequences for Production of TITLE OF INVENTION: 2,4-Diacetylphloroglucinol and Methods
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             400 cccgtccggcgtaatcttccggtggtcggaaaacttcccgattccatcaaaggagtgtat 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 788 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                               TOPOLOGY:
                                                                                                                                                                                             NAME: Connor, Margaret A REGISTRATION NUMBER: 300
                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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Weller, David M
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                                linear
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             DNA (genomic)
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                                                                                                                                                                                 0009.95
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; LOCATION: complement (1..1047); OTHER INFORMATION: /note= "phiD DNA sequence. SEQ ID; OTHER INFORMATION: NO:12 is translation (protein) of SUS-08-494-907-11
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PCT-US96-10986-11/c
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                                                                                                                               REFERENCE/DOCKET NUMBER: A700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (813) 289-2966
TELEFAX: (813)289-2967
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1047 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application PC/TUS9610986
GENERAL INFORMATION:
TITLE OF INVENTION: Sequences for Production of
TITLE OF INVENTION: 2,4-Diacetylphloroglucinol and Methods
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephan A. Pendorf, DOMINIK & STEIN
STREET: 600 N. West Shore Boulevard, Suite 1000
                                                               TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE:
ORIGINAL SO
                               ANTI-SENSE:
                                              HYPOTHETICAL:
                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Pendorf, Stephan A
REGISTRATION NUMBER: 326
                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                 ORIGINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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STREET: U.STREET: Tampa
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                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
ZIP: 33609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                               STRANDEDNESS:
                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
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Local Similarity 48.2%;
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                 SOURCE:
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                                                                                   linear
Pseudomonas fluorescens
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                                                                 DNA (genomic)
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RESULT 12
5225348-2
;Patent NO. 5225348
;Patent NO. 5225348
;Patent NO. 5225348
;UETSUKI, TAICHI;KAZIRO, YOSHITO
;UETSUKI, TAICHI;KAZIRO, YOSHITO
;TITLE OF INVENTION: DNA FRAGMENT AND EX
;CONTAINING THE DNA FRAGMENT
;UNMBER OF SEQUENCES: 9
;CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/447,823
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5225348-2
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; OTHER INFORMATION:
; OTHER INFORMATION:
PCT-US96-10986-11
                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:2:
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Best Local S
Matches 94
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Best Local Similarity
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NAME/KEY:
1317 ccacctttgggtcgc 1331
                                                                                              460
                                                                                                                                           400 cccgtccggcgtaatcttccggtggtcggaaacttcccgattccatcaaaggagtgtat 459
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                     520 gacggtatggttcac 534
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                                                                                                                         attgatcgccgttctggtaaaaagctggaagatggccctaaattcttgaagtctggtgat 1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tggccggttattggc 779
                                                                             gtgcgcaacggagctaacccacttcacgagccggtgacaggtcaccacttcttcgacgga 519
                                                                                                                                                                                       cctgtattggattgccacacggctcacattgcatgcaagtttgctgagctgaaggaaaag 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGCATGTCTTCAATCGCCGCGCGCCAGGCCATTGAAAAACGCGGGCTTGACCACGGACGA 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cggtatagtcgacccggcacacggaaccggtgtagctaacgccggtttggtctatttcaa 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tgagcttcacggccacaccggtattgcccgactcatgctattctacgccagagctgcagc 704
                                                           gctgccattgttgatatggttcctggcaagcccatgtgtgttgagagcttctcagactat 1316
                                                                                                                                                                                                                                                    94;
                                                                                                                                                                                                                                                    Conservative
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RMATION: /note= "phlD DNA sequence.
RMATION: NO:12 is translation (prot
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                                                                                                                                                                                                                                                   Score 33.4; DB 6; Length 1
Pred. No. 1.2;
0; Mismatches 101; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXPRESSION PLASMID
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(protein)
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US-08-494-907-1/c

Sequence 1, Application US/08494907
Patent No. 5955298
GENERAL INFORMATION:
APPLICANT: Thomashow, Linda S
APPLICANT: Bangera, Mahalaxmi

В Qy

Best Local Similarity 48.7 Matches 94; Conservative

48.28;

Pred. No. 1.9; 0; Mismatches

101;

Indels

0;

Gaps

0

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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-494-907-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEBEAX: (510) 559-60
TELEBEAX: (510) 559-5777
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3680 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: ""
TYPOTHFTT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AOLECULE N
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Connor, Margaret A
REGISTRATION NUMBER: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Sequences for Production of TITLE OF INVENTION: 2,4-Diacetylphloroglucinol and Methods
                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Weller, David MAPPLICANT: Cook, R. James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 800 E
CITY: Albany
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                                                    NAME/KEY:
                                                                                                                                                                                                     NAME/KEY: misc_feature LOCATION: complement (; OTHER INFORMATION: /not OTHER INFORMATION: rig]
                                                                                                                                                                                                                                                                                        LOCATION: complement (1689..2855)
OTHER INFORMATION: /note= "phlC, transcribed from OTHER INFORMATION: right to left"
                                                                                                                                                                                                                                                                                                                                                                              LOCATION: complement OTHER INFORMATION: /I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: complement (
OTHER INFORMATION: /no
                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 2118..3371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                    OTHER INFORMATION:
                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                            misc_feature
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                                                                                  misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
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                                                                                                      to right"
                              /note= "SEQ ID NO:1 contains genes
necessary for Phl synthesis."
                                                                                                                                                                                                     /note= "phlD, "
right to left"
                                                                                                                                                                                                                                                                                                                                                                         nt (1210..1917)
/note= "phlB, transcribed from
right to left"
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/note= "phlA, transcribed from
right to left"
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Query Match

1.98;

Score 33.4;

DB 2;

Length 3680;

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PCT-US96-10986-1/c
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GENERAL INFORMATION:
TITLE OF INVENTION: Sequences for
TITLE OF INVENTION: 2,4-Diacetylp)
                                                                                                                                                                                                                                                                                                                                             TELEFAX: (813)289-2967
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3680 base pairs
                                                                                                                                                                                                                                                                    MOLECULE TYPE: D
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF STEVENIER STEIN CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephan A. Pendorf, DOMINIK & STEIN PROPERT: 600 N. West Shore Boulevard, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: A7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (813) 289-2966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                       FEATURE:
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                                                                                                                                 NAME/KEY: misc_feature
LOCATION: complement (2889..3680)
OTHER INFORMATION: /note= "phla,
                                OTHER INFORMATION: OTHER INFORMATION:
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 NAME/KEY:
                                                                     LOCATION:
                                                                                   NAME/KEY: misc_feature
                                                                                                                        OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Pendorf, Stephan
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misc_feature
                                complement (1210..1917)
WMATION: /note= "phlB, "
WMATION: right to left"
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                                                                                                                                                                                                                                                               NO
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LOCATION: misc_feature
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OTHER INFORMATION: /note=
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US-08-494-907-2/c
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Best Local S
Matches 94
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                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,907
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CONDOY, MARGARET A
REGISTRATION NUMBER: 30043
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OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Sequences for Production of TITLE OF INVENTION: 2,4-Diacetylphloroglucinol and Methods NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Thomashow, Linda S APPLICANT: Bangera, Mahalaxmi APPLICANT: Weller, David M APPLICANT: Cook, R. James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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STATE: CA
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LOCATION:
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les 94; Conservative
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INFORMATION: /note= "phlc,"
INFORMATION: right to left"
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2118..3371
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/note= "phlD, t
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to right"
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necessary for Phl synthesis."
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; NAME/KEY: misc_feature
; LOCATION: 1..5076
; OTHER INFORMATION: /note
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US-08-494-907-2
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5076 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 94; Conserv
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NAME/KEY: misc_feature
LOCATION: 3514..4767
OTHER INFORMATION: /note
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2154
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                                                                                                                                                                                               2334 GGCTAAACGGATGATTCAAAACACCCAAGTCAATGAACGGTATCTGGTCTTGCCCCATCGA 2275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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ORGANISM: Pseu
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                              765
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LOCATION: complement (2..1270)
OTHER INFORMATION: /note= "phl
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OTHER INFORMATION: /note= "phlD, oTHER INFORMATION: right to left"
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OTHER INFORMATION: /note= "phlC,
OTHER INFORMATION: right to left"
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LOCATION: complement (2606...3313)
OTHER INFORMATION: right to left"
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LOCATION: complement (4285..5076)
OTHER INFORMATION: /note= "phla, to
OTHER INFORMATION: right to left"
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CATCCGGATGGTCGC 2140
                                                                                                                                                                                                                tgagcttcacggccacaccggtattgcccgactcatgctattctacgccagagctgcagc 704
                         tggccggttattggc 779
                                                               CCGCATGTCTTCAATCGCCGCGCCCAGGCCATTGAAAACGCGGGCTTGACCACGGACGA 2155
                                                                                 cggtatagtcgacccggcacacggaaccggtgtagctaacgccggttttggtctatttcaa 764
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559-5777
                                                                                                                                                                                                                                                                            1.98;
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to right"
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                                                                                                                                                                                                                                                                                                                                                                           /note= "SEQ ID NO:2 contains genes involved in synthesis, activity, a
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Search completed: July 24, 2002, 06:21:27 Job time: 8847 sec

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Listing first 45 summaries
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O1-OCT-2000 (TrembLrel. 15, Created)
O1-OCT-2000 (TrembLrel. 15, Last sequence update)
O1-DEC-2001 (TrembLrel. 19, Last annotation update)
O1-DEC-2001 (TrembLrel. 19, Last annotation update)
9-CIS-EPOXYCAROTENOID DIOXYGENASE (NEOXANTHIN CLEAVAGE ENZYME).
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid eurosids II, Brassicales; Brassicaceae; Arabidopsis.
         Submitted (APR-1999) to the EMBL; AB028617; BAB01336.1; EMBL; AB026549; BAB70609.1; InterPro; IPR004294; RPE65. pfam; PF03055; RPE65; 1.
                                                                                  Iuchi S., Kobayashi M., Shinozaki K.;
"Characterization of neoxanthin cleav
thaliana.";
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MEDLINE-20277480; PubMed-10819329;
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                                                                                                                                                            DNA Res. 7:131-135(2000).
[3]
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Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;

"Full Length cDNA of reportation."
                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eu eurosids II; Brassicales; Brassicaceae; Arabidopsis. NCBL_TaxID=3702;
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T 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
T 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
T 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Matches
Burbidge A., Taylor I.B., Thompson A.;
"Potato putative 9-cis-epoxycarotenoid
Submitted (MAR-2000) to the EMBL/GenBan
EMBL; AJ276244; CAB76920.1; -.
Interpro; IPR004294; RPE65.
Pfam; PF03055; RPE65; 1.
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Best Local Similarity 71.3%;
Matches 432; Conservative
SEQUENCE FROM N.A.

SEQUENCE FROM N.A., Jackson A., Thompson A., Taylor I.B.;
Burbidge A., Grieve T.M., Jackson A., Thompson A., Taylor I.B.;
"Structure and expression of a cDNA encoding a putative neoxanthin cleavage enzyme (NCE) isolated from a wilt-related tomato (Lycopersicon esculentum Mill.) library.";
J. Exp. Bot. 47:2111-2112(1997).
                                                                                                                                                                                                                  Lycopersicon esculentum (Tomato).
Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Pred. No. 7.6e-174;
6; Mismatches 90;
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InterPro; IPR004294; RPE65.
Pfam; PF03055; RPE65; 1.
Dioxygenase.
SEONERGY
                Q9M9F5 PRELIMINARY; PRT; 657 AA.
Q9M9F5;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
F3F9.10.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
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RAPARA RA

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Query Match 68.9%;
Best Local Similarity 67.7%;
Matches 419; Conservative 8
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EMBL; AC013430; AAF71797.1; -
ENBL; AC013430; GRAM_POS_ANCHORING; UNKNOWN_1.
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O Q., Brooks S., B
on P., Altafi H.,
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LYGDNRYGGEPLFLPGEGGEEDEGYILCFVHDEKTWKSELQIVNAVSLEVEATVKLPSRV
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Iuchi S., Kobayashi M., Yamaguchi-Shinozaki K., Shinozaki K.;
"A stress-inducible gene for 9-cis-epoxycarotenoid dioxygenase involved in abscisic acid biosynthesis under water stress in drtolerant cowpea.";
Plant phant compea.";
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EMBL; AB030293; BAB11932.1; -.
SEQUENCE 612 AA; 67715 MW; E3
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9-CIS-EPOXYCAROTEUNTT
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Qin X., Zeevaart J.A.;
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                    IDAPDCFCFHLWNAWEEPETDEVVVIGSCMTPPDSIFNESDENLKSVLSEIRLNLKTGES
                                                                                                                                                                                                                                                                                        YEPVAGHHFFDGDGMVHAVKFTNGAASYACRFTETQRLAQEKSLGRPVFPKAIGELHGHS
                                                                                                                                                                                                                                                                                                                                                             TALVSHESKHPLPKTADPKVQIAGNFAPVPEHAADQALPVVGKIPKCIDGVYVRNGANPL
   IDAPECFCFHLWNAWEEPETDEIVVIGSCMTPADSIFNECDESLKSVLSEIRLNLRTGKS
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69.2%;
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15,
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Pred. No. 6e-1
9; Mismatches
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95;
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Phaseolus.
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                                     461
                                                                                                          401
                                                                                                                                                                             341
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RESULT
Q9AXZ4
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Best Local 9
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"Abscisic acid in avocado fruit.";

"Abscisic acid in avocado fruit.";

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ

EMBL; AF224671; AAR00623.1; -.

InterPro; IPR000221; Protamine_P1.

PROSITE; PS00048; PROTAMINE_P1; UNKNOWN_1.
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dioxygenase.
SEQUENCE (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Persea americana (Avocado).
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
NCBI_TaxID=3435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9-CIS-EPOXYCAROTENOID
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                                   ADPSVQIAGNEAPVNEQPVRRNLPVVGKLPDSIKGVYVRNGANPLHEPVTGHHFFDGDGM 176
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                                                                                                                                                                                                                                                                                                                  NSPATVVKPKAKESNTKQ----
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                                                                                                                                                            IVDPAHGTGVANAGLVYFNGRLLAMSEDDLPYQVQITPNGDLKTVGRFDFDGQLESTMIA
                                                                                                                                                                                                                                        ADPEVQIAGNEAPVAEHPVQHGIPVAGRIPRCLDGVYVRNGANPLFEPIAGHHFFDGDGM
                                                                                                                                                                                                                                                                                         LTPSIEKNPGSHQVKTDQSGPNRVGPNWNIFQRTAAFALDAIEEKLIARVLERRHPLPKT
                                                                                                                                                                                                                                                                                                                                           LPISKNLSRPKNFIMLKHNTPLIQCCSHSPSSSSAAVLHLPPKQPTKSKPSIKKGEKSST
                                                                                                                                                                                                                                                                                                                                                                                            392;
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625
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          69724 MW;
                                                                                                                                                                                                                                                                                                                                                                                                        65.6%;
64.9%;
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ta; Laurales;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 2066.5; DB 1
Pred. No. 4.4e-156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          A56F33042D5F2CB6
                                                                                                                                                                                                                                                                                                        -MNLFQRAAAAALDAAEGFLVSH--EKLHPLPKT 116
                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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RA MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Gill J.E., Goldsmith A.D., Hass B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Lingin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Militscher J., Miranda M., Nguyen M., Rooney T., Rowley D.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
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Best Loc
Matches
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
9-CIS-EPOXYCAROTENOID DIOXYGENASE, PUTATIVE.
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Local (
                                                                                                                                                            87
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                         DSIKGVYVRNGANPLHEPVTGHHFFDGDGMVHAVKFEHGSASYACRFTQTNRFVQERQLG
                                                                                                                                                                                                                                                 SQSSDLSYCSSLPMASRVTRKLNVSSALHTPPALHFPKQSSNSPAIVVKPKAKESNTKQM
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DCIDGVYLRNGANPLFEPVSGHHLFDGDGMVHAVKITNGDASYSCRFTETERLVQEKQLG
                                                                                                         NPLQRAASAALDFAETALLRRERSKPLPKTVDPRHQISGNYAPVPEQSVKSSLSVDGKIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC074176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    408:816-820(2000).
AC074176; AAG50855.1;
                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  597
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                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65336 MW;
                                                                                                                                                                                                                                                                                                                                                     64.9%;
                                                                                                                                                                                                                                                                                                                              69;
                                                                                                                                                                                                                                                                                                                           Score 2044.5;
Pred. No. 2.3e
69; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              6A79B2BF7EAA8179 CRC64;
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edons; core e
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.3e-154;
les 101; I
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                                                                                                                                                                                                                                                                                                                                                                            Length
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Query Match
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Matches 380
                                                       EU Arabidopsis sequencing pro
Submitted (MAR-2000) to the E
EMBL; ALC21710: CAA15715.1; -
EMBL; AL161548: CAB78837.1; -
InterPro; IPR004294; RPE65.
Pfam; PF03055; RPE65; 1.
SEQUENCE 583 AA; 65066 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 O49505;
01-JUN-1998
01-JUN-1998
                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence up
01-JEC-2001 (TrEMBLrel. 19, Last annotation
NEOXANTHIN CLEAVAGE ENZYME-LIKE PROTEIN.
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                                                                                                                                                                       SEQUENCE FROM N.A.
Hilbert H., Braun M.,
Mewes H.W., Lemcke K.,
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PYQVRVTDNGDLETIGRFDFDGQLSSAMIAHPKIDPVTKELFALSYDVVKKPYLKYFKFS
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Hilbert H.,
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          . 2%
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  82;
Score 1991; D
Pred. No. 4.1e
82; Mismatches
                                                                                                                                                            r E., Brandt A., Du
r K.F.X.;
EMBL/GenBank/DDBJ
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EMBL/GenBank/DDBJ
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                                                        A138F93542E50852
           1991;
No. 4.
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DB 10;
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  22;
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Gaps
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GGNHTQPPLSSSQSSDLSY--CSSLPMASRVTRKLNVSSALHTPPALHFPKQSSNSPAIV

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Best Local S
Matches 373
                                                                                                                             Chernys J., Zeevaart J.A.D.; "Abscisic acid biosynthesis Submitted (JAN-2000) to the EMBL; AF224672; AAK00632.1;
                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                            Q9AXZ3;
                                                                                                                                                                                                            Eukaryota; Viridiplantae; Str
Spermatophyta; Magnoliophyta;
                                                                                                            Dioxygenase.
SEQUENCE 5
                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-CV. LULA;
                                                                                                                                                                                                                                                      9-CIS-EPOXYCAROTENOID
                                                                                                                                                                                                    NCBI_TaxID=3435;
                                                                                                                                                                                                                                 Persea americana (Avocado)
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                    KTFTIHSSLHSSPVLHLPKLLTTTTPLHEKSQRELGLIL---
                               RKLNVSSALHTPPALHFPK------
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AALDAAEGFLVSH--EKLHPLPKTADPSVQIAGNFAPVNEQPVRRNLPVVGKLPDSIKGV
                                                         al Similarity 65.9
373; Conservative
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yta; Laurales;
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EMBL/GenBank/DDBJ databases
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Last sequence up
Last annotation
                                                           Score 1977; DB 10;
Pred. No. 5.2e-149;
6; Mismatches 97;
                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                            CD12075EE9022461 CRC64;
                                       -QSSNSPAIVVKPKAKESNTKQMNLFQRAAA
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Lauraceae; P
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Best Local
Matches 37
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01-JAN-1998
01-JAN-1998
01-DEC-2001
                                                                                                                                                                                                                                                         Zea mays (Maize).

Bukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Panicoldeae; Andropogoneae; Zea.

NCBI_TaxID=4577;
                                                                                                                                                                 MEDLINE=98004553; PubMed=9342392;
Tan B.C., Schwartz S.H., Zeevaart J.A., McCarty D.R
"Genetic control of abscisic acid biosynthesis in m
Proc. Natl. Acad. Sci. U.S.A. 94:12235-12240(1997).
EMBL, U95953; AAB62181.1; -
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                                                                                                                                    InterPro; IPR004294; RPE65.
Pfam; PF03055; RPE65; 1.
SEQUENCE 604 AA; 65587 M
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-KPKAKESNTKOMNLFQRAAAAALDA-AEGFLVS-HEKLHPLPKTADPSVQIAGNFAPVN
                                   PARSRARAS----NSVRFSPRAVSSVPPAECLQAPFHKPVADLPAPSRKPAAIAVPGHA
                                                       PPLSSSQSSDLSYCSSLPMASRVTRKLNVSSALHTP---PALHFPKQSSNSPATVV----
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                                                                             Similarity 63.75; Conservative
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3 (TrEMBLrel.
(TrEMBLrel.
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63.3%;
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Last sequence update)
Last annotation updat
                                                                             Score 1930; D
Pred. No. 3.2e
73; Mismatches
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a; Poales; Poaceae; PACC
                                                                             DB 10;
1.2e-145;
nes 122;
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RESULT
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                                                       Query Match
Best Local Similarity
Matches 323; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O9LRM7;
01-OCT-2000 (TrEMBLrel. 15, Create 01-OCT-2000 (TrEMBLrel. 15, Last s 01-OCT-2000 (TrEMBLrel. 15, Last a 9-CIS-EPOXYCAROTENOID DIOXYGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thallana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopsis spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                       Dioxygenase
SEQUENCE
                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=COLUMBIA;
Sato S., Nakamura Y.,
Submitted (JUN-1999)
                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                 clones.
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                                                                                                                                                                                                                                                                                             Nakamura
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                                                                                                                                                                                                                                                       features
                                                                                                                                                                                                                                                                       Structural
                                                                                                                                                                                                                                                                                                         MEDLINE-20277480; PubMed-10819329;
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRFTETARLRQERAIGRPVFPKAIGELHGHSGIARLALFYARAACGLVDPSAGTGVANAG
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.s. 7:131-135(2000).
AR028621; BAB01363.1;
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                                                                                                                                                         577
                                                           Conservative
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                                                                                                                                                       MW;
                                                       s; score 1663.5; DB 10; Pred. No. 5.2e-124; 100; Mismatches 137;
                                                                                                                                                                                                                                                       4,504,864
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                                                                                                                                                                                                                                                                                                                                                                                     T., Kato T., Asan
EMBL/GenBank/DDBJ
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                                                                             1663.5;
No. 5.2e
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DBJ databases
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RESULT
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ID 49672
ID 207
O2 04
D1 01
D1 01
D1 01
O2 06
O2 07

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SEQUENCE FROM P
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049675;
01.JUN-1998 (TrEMBLrel. 06, Created)
01.JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEOXANTHIN CLEAVAGE ENZYME-LIKE PROTEIN (AT4G19170/T18B16_140).
T18B16.140 OR AT4G19170.
                        SEQUENCE FROM N.A.
Cheuk R., Chen H., Kim C.J.,
Bowser L., Carninci P., Dale
Ishida J., Jiang P.X., Jones
                                                                                                                                                                                                                                                            Benes V.,
Mayer K.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T18816.140 OR ATBLIAN.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta;
Eukaryota, Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
                                                                                                                                                                                                                                                                                                                                                            BEQUENCE FROM N.A.
Bevan M., Benes V., Rechmann S., E
Mewes H.W., Mayer K., Schueller C.
Submitted (JAN-1998) to the EMBL/C
                                                                                                                                            EU Arabidopsis sequencing project; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                           SEQUENCE
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J.M., Goldsmith A.D., Hayashizaki
T., Kaniya A., Karlin-Neumann G.,
Lin J., Liu S.X., Miranda M., Narus
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                                                                                                                                Q94IR2 PRELIMINARY; PRT; 543 AA.
Q94IR2;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CARCOTENOID 9,10-9',10' CLEAVAGE DIOXYGENASE.
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                   Phaseolus vulgaris (Kidney bean) (French bean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseol
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Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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Search completed: July 19, 2002, 10:15:43 Job time: 235 sec

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Copyright (c) 1993 - 2000 Comp
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ALIGNMENTS

AAE04784 ID AAE(

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AAE04784 standard; Protein;

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AAE04784;

10-SEP-2001

(first entry)

Neoxanthin cleavage enzyme; AtNCED3; abscisic acid; ABA; herbicide; stress tolerance; transgenic plant; plant breeding; antisense-therapy; plant growth protectant. WPI; 2001-400081/43. N-PSDB; AAD09396. (RIKE) RIKEN KK. 13-JAN-2000; 2000JP-0010056. 11-JAN-2001; 2001JP-0003476 Arabidopsis thaliana. Arabidopsis thaliana neoxanthin cleavage enzyme, AtNCED3. Iuchi S, 11-JAN-2001; 2001EP-0300218 18-JUL-2001. EP1116794-A2. Kobayashi × Shinozaki K;

Neoxanthin cleavac

A DNA encoding a protein with a neoxanthin cleavage activity for producing transgenic plants with improved or decreased stress tolerance

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to neoxanthin cleavage enzymes and their corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key role in endogenous abscisic acid (ABA) biosynthesis under drought stress. Neoxanthin cleavage enzyme is used for improving stress tolerance in a
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                                                 edegyilcfvhdektwkselgivnavsleveatvklpsrvpygfhgtfigaddlakqvv
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RESULT AAE04789 ID AAE(

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Best Local
                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                             corresponding CDNA molecules. Neoxanthin cleavage enzyme plays a key role in endogenous abscisic acid (ABA) biosynthesis under drought stress. Neoxanthin cleavage enzyme is used for improving stress tolerance in a plant when expressed in a plant cell. The invention also relates to methods for increasing or decreasing stress tolerance in a plant by introducing the DNA into the plant, and a transgenic plant into which a neoxanthin cleavage enzyme is introduced. The improvement of stress tolerance in plants is useful, for example in plant breeding. Neoxanthin cleavage enzyme genes are useful for example in plant breeding. Neoxanthin cleavage enzyme years and then removing the weed by specifically lowering stress tolerance in the weed by inducing an inducible promoter. The present sequence is Lycopersicon esculentum neoxanthin cleavage enzyme, LeNCED1 protein related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A DNA encoding a protein with a neoxanthin cleavage activity for producing transgenic plants with improved or decreased stress tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tomato; neoxanthin cleavage enzyme; LeNCED1; abscisic acid; ABA; stress tolerance; transgenic plant; plant breeding; antisense-therapy; plant growth protectant; herbicide.
                                                                                                                                                                                                                                                                                                                   Sequence
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11-JAN-2001;
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2001-400081/43
DB; AAD09401.
                                                                                                                                     FPKQSSN--SPA--IVVKPKAKESN-----TKQMNLFQRAAAAALDAAEGFLVSHEKLHP 112
                                                                                                                                                                               tttshatntwi-----ktklsmpsskefgfasnsisllknghnrgslninsslgappilh 57
                                                                            LPKTADPSVQIAGNFAPVNEQPVRRNLPVVGKLPDSIKGVYVRNGANPLHEPVTGHHFFD 172
                                                                                                                                                                                                            TATAAVSGRWLGGNHTQPPLSSSQSSDLSYCS---SLPMASRVTRKLNVSSALHTPPALH 61
                                                         lpktadprvqisgnfapvpenpvcqslpvtgkipkcvqgvyvrnganplfeptaghhffd
                                                                                                                  fpkqssnyqtpknntishpkqennnssssstskwnlvqkaaamaldavesaltkhelehp 117
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2001JP-0003476
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71.78;
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                                                                                                                                                                                                                                        Score 2280.5;
Pred. No. 4.4e
53; Mismatches
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ARESULT AABF 2308 ID AABF 2308 ID AABF 2308 KW NCE: WW NCE: WW
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                                                                                                                                                          Novel isolated defence-related signalling gene isolated from sunflower encoding neoxanthin cleavage enzyme, amino acid permease or glutamic acid-rich protein useful for increasing resistance of plant to a
This invention relates to defence-related signalling genes isolated from the sunflower (Helianthus annuus). The genes encode a neoxanthin cleavage enzyme (NCE), an amino acid permease (AAP) and a glutamic acid rich protein (GRP). The signalling gene is useful for increasing the
                                                                                                                                                                                                                                                                                                                                 (PION-)
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23-MAY-2000;
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d rich protein; GRP;
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Pred. No. 4.4e-222;
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Matches 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     corresponding CDNA molecules. Neoxanthin Cleavage enzyme plays a key role in endogenous abscisic acid (ABA) biosynthesis under drought stress. Neoxanthin cleavage enzyme is used for improving stress tolerance in a plant when expressed in a plant cell. The invention also relates to methods for increasing or decreasing stress tolerance in a plant by introducing the DNA into the plant, and a transgenic plant into which a neoxanthin cleavage enzyme is introduced. The improvement of stress tolerance in plants is useful, for example in plant breeding. Neoxanthin cleavage enzyme genes are useful for producing transgenic plants. An arid land can be improved by growing transformant weed for several years and then removing the weed by specifically lowering stress tolerance in the weed by inducing an inducible promoter. The present sequence is Vigna unguiculata neoxanthin cleavage enzyme, CPRD65 (Cowbea Responsive to Dehydration) protein. CPRD65 gene is isolated from cowpea plant.
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corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key role in endogenous abscisic acid (ABA) biosynthesis under drought stress Neoxanthin cleavage enzyme is used for improving stress tolerance in a plant when expressed in a plant cell. The invention also relates to methods for increasing or decreasing stress tolerance in a plant by introducing the DNA into the plant, and a transgenic plant into which a

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                           Maize; neoxanthin cleavage enzyme; VP14; abscisic acid; ABA; herbicide; stress tolerance; transgenic plant; plant breeding; antisense-therapy;
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Pred. No. 1.7e-186;
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           CC This invention relates to defence-related signalling genes isolated from CC the sunflower (Helianthus annuus). The genes encode a neoxanthin cleavage CC enzyme (NCE), an amino acid permease (AAP) and a glutamic acid rich CC protein (GRP). The signalling gene is useful for increasing the CC resistance of a plant to a pathogen such as fungus, virus, bacterium, CC nematode or insect (e.g. European corn borer), preferably (CC construct containing the gene into the genome of the plant. The gene is CC useful for regulating gene expression in a plant, in response to a CC stimulus such as infection with a pathogen, damage from a pathogen, CC hydrogen peroxide, jasmonic acid, methyl jasmonate, salicylic acid, coxalic acid or expression of a gene encoding oxalic acid oxidase. The genes are also useful for stem-preferred regulation of gene expression in a plant. The genes are useful in agriculture, particularly in the breeding of crop plants with improved agronomic traits, for modifying abscisic acid (ABA) metabolism and for modifying amino acid transport and content in plants. The present sequence represents a neoxanthin cleavage of the content in plants. The present sequence represents an examination of content and content in plants. The present sequence represents an examination of content and content in plants. The present sequence represents a neoxanthin cleavage content in plants. The present sequence represents a neoxanthin cleavage content in plants. The present sequence represents a neoxanthin cleavage content in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated defence-related signalling gene isolated from sunflower encoding neoxanthin cleavage enzyme, amino acid permease or glutamic acid-rich protein useful for increasing resistance of plant to a
sunflower NCE
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stress tolerance; transgeni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                              KFAYLALAEPWPKVSGFAKVDLTTGEVKKHLYGDNRYGGEPLFLPGEGGE----EDEGY 545
                                                                                                                                                                                                                                                                                                              ILCFVHDEKTWKSELQIVNAVSLEVEATVKLPSRVPYGFHGTFIGADDLAKQ
                                                                                                                                                                                                                                                                                                                                                                                                MTPPDSIFNESDENLKSVLSEIRLNLKTGESTRRPIISNEDQQVNLEAGMVNRNMLGRKT 490
                                                                                                                                                                                                                                                                                                                                                                                                                                  RGGSPVVYDKNKVARFGILDKYAEDSSNIKWIDAPDCFCFHLWNAWEEPETDEVVVIGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQPVRRNLPVVGKLPDSIKGVYVRNGANPLHEPVTGHHFFDGDGMVHAVKFEHGSA-SYA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aaprkaeggkkqlnlfqraaaaaldafeegfvanvlerphglpstadpavqiagnfapvg 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -KPKAKESNTKQMNLFQRAAAAALDA-AEGFLVS-HEKLHPLPKTADPSVQIAGNFAPVN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLSSSQSSDLSYCSSLPMASRVTRKLNVSSALHTP---PALHFPKQSSNSPAIVV----
                                                                                                                                                                                                                                                                                                                                 ryaylavaepwpkesgfakedlstgeltkfeygegrfggepcfvpmdpaaahprgeddgy
                                                                                                                                                                                                                                                                                                                                                                            mtpadsifnesderlesvlteirldartgrstrravlp-psqqenlevgmvnrnllgres
                                                                                                                                                                                                                                                                                                                                                                                                                     rggspvvldkektsrfgvlpkhaadasemawvdvpdcfcfhlwnawedeatgevvvigsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVYFNGRLLAMSEDDLPYQVQITPNGDLKTVGRFDFDGQLESTMIAHPKVDPESGELFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erppvhelpvsgrippfidgvyarnganpcfdpvaghhlfdgdgmvhalrirngaaesya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                parsraras----nsvrfspravssvppaeclqapfhkpvadlpapsrkpaaiavpgha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                      604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                        2001EP-0300218
        2000JP-0010056
2001JP-0003476
                                                                                                                                                                                          (first entry)
                                                                                                                                       transgenic
                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73;
                                                                                                                                      AtNCED5; abscisic acid; c plant; plant breeding;
                                                                                                                                                                                                                                      577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1930; DB 22;
Pred. No. 1.7e-186;
3; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                       :
:
:
                                                                                                                                                                    cleavage enzyme,
                                                                                                                                                                                                                                     A
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                                                                                                                                                                     AtNCED5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                ABA; herbicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ···
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                604;
                                                                                                                                                                                                                                                                                                              597
                                                                                                                                                                                                                                                                                         602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191
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                                                                                                                                                                                                                                                                                                                                                                                                                      431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250
```

expression control;

promoter; pathway; NO:

37612

Claim

576

598

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CC corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key crole in endogenous abscisic acid (ABA) biosynthesis under drought stress. CC Neoxanthin cleavage enzyme is used for improving stress tolerance in a cc plant when expressed in a plant cell. The invention also relates to introducing the DNA into the plant, and a transgenic plant into which a cheoxanthin cleavage enzyme is introduced. The improvement of stress concernation of the DNA into the plant, and a transgenic plant into which a cc neoxanthin cleavage enzyme is introduced. The improvement of stress cc cleavage enzyme genes are useful, for example in plant breeding. Neoxanthin cleavage enzyme genes are useful for producing transgenic plants. An arid clarance in mproved by growing transformant weed for several years and cc then removing the weed by specifically lowering stress tolerance in the ceed by inducing an inducible promoter. The present sequence is Cc weed by inducing an inducible promoter. The present sequence is Cc Arabidopsis thaliana neoxanthin cleavage enzyme, AtNCED5 protein. CC The AtNCED5 cDNA is obtained from an Arabidopsis plant-derived cDNA cc gene isolated from cowpea plant as a probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 323; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A DNA encoding a protein with a neoxanthin cleavage activity for producing transgenic plants with improved or decreased stress tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAD09398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RIKE ) RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                    VGKLPDSIKGVYVRNGANPLHEPVTGHHFFDGDGMVHAVK--FEHGSASYACRFTQTNRF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSSSQSSDLSYCSSLPMASRVTRKLNVSS-ALHTPPALHFPKQSSNSPAIVVKPKAKESN 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-400081/43.
                                                                                                                                                  KNKVARFGILDKYAEDSSNIKWIDAPDCFCFHLWNAWEEPETDE----VVVIGSCMTPPD
                                                                                                                                                                                                                                                             VQERQLGRPVFPKAIGELHGHTGIARLMLFYARAAAGIVDPAHGTGVANAGLVYFNGRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \verb|aiadpwpkcsgiakvdiqngtvsefnygpsrfggepcfvpegegeedkgyvmgfvrdeek|
                  ALAEPWPKVSGFAKVDLTTGEVKKHLYGDNRYGGEPLFLPGEGGEEDEGYILCFVHDEKT
                                                                                    SIFNESDENLKSVLSEIRLNLKTGESTRRPIISNEDQQVNLEAGMVNRNMLGRKTKFAYL:||:|| | | : ||::|| |::||::|| |::
                                                                                                                               kekmarfgvlskqdltgsdinwvdvpdcfcfhlwnawee-rteegdpvivvigscmsppd
                                                                                                                                                                                               LKYFRFSPDGTKSPDVEIQLDQPTMMHDFAITENFYVVPDQQVVFKLPEMIRGGSPVVYD 379
                                                                                                                                                                                                                                                                                                                              tifsesgeptrvelseirlnmrtkesnrkvivtg----vnleaghinrsyvgrksqfvyi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---Inllqklaatmldkiessivipmegnrplpkptdpavqlsgnfapvnecpvqnglev 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   llptktsprshllpqpknanisrrilinpfkiptlpdltspvpsp-----vklkptypn
                                                                                                                                                                                                                                                                                                                                                                                                   vgqipsclkgvyirnganpmfpplaghhlfdgdgmihavsigfdn-qvsyscrytktnrl 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig 10; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kobayashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       577 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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55.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1663.5; DB 2:
Pred. No. 1.8e-159;
)0; Mismatches 137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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                                                                                                   495
                                    555
                                                                   473
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AAG31333
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               25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
24-MAR-1999
06-APR-1999
06-APR-1999
07-APR-1999
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08-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
24-AMY-1999
06-MAY-1999
06-MAY-1999
07-MAY-1999
11-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      termination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hybridisation assay; genetic mapping; gene termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     identification; signal transduction pathway; metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
990S-0126264
990S-0128734
990S-0128734
990S-0128734
990S-0130449
990S-0130489
990S-0132485
990S-0132486
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990S-0132486
990S-0134218
990S-0134218
990S-0134221
990S-0134720
990S-0134730
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990S-0134844
990S-0137724
990S-0138844
990S-0138844
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474 496 418 436 359 380 320 239

299

179

200

260

120 142

63 83

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Qy
                       В
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                                                                                        Query Match
Best Local Sin
Matches 210;
                                                                                     13-AUG-1999
16-AUG-1999
17-AUG-1999
20-AUG-1999
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27-AUG-1999
27-AUG-1999
31-AUG-1999
32-SEP-1999
33-AUG-1999
31-AUG-1999
32-COT-1999
         102
                        42
                                       42
GFLVSHEKLHPLPKTADPSVQIAGNFAPVNEQPVRRNLPVV-GKLPDSIKGVYVRNGANP
                      imi
                                                     30.7%; Score ilarity 36.7%; Pred. Conservative 106; Mis
                                                                                    9908-0148684
9908-0149175
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                                                     e 968; DB
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lismatches
                                                     21;
-89;
220;
                                                      Indels
                                                      36;
                                                      Gaps
         160
                        94
                                       101
                                                       13;
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17.JUN-1999
18.JUN-1999
19.JUN-1999
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27.JUN-1999
27.JUN

-0139452 -0139453 -0139453 -0139459 -0139459 -0139463 -0139963 -0139963 -0140025 -01400

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RRESULT 1
AABE04783
AID AAABA
XX AABC
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KW Neo
KW Stre
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                                                                                                                A DNA encoding a protein with a neoxanthin cleavage activity for producing transgenic plants with improved or decreased stress tolerance
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                              Example 10;
                                                                                                                                                                                                       N-PSDB; AAD09395
                                                                                                                                                                                                                                                                                                                                                (RIKE ) RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                         13-JAN-2000; 2000JP-0010056
11-JAN-2001; 2001JP-0003476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JAN-2001; 2001EP-0300218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-SEP-2001
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plant breeding;
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RESULT 1 AAB72306

AAB72306 standard; Protein;

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16-MAY-2001

(first entry)

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The AtNCED2 cDNA is obtained from an Arabidopsis plant-derived cDNA clibrary using a cDNA of the CRRD55 (CowPea Responsive to Dehydration) covered is considered from cowpea plant as a probe.
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                                   S--LEVEATVKLPSRVPYGFHGTFIGADDLAK 596
                                                                                                                                                                                             E----VKKHLYGDNRYGGEPLFLPGEGG----EEDEGYILCFVHDEKTWKSELQIVNAV
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Pred. No. 8.3e-89;
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                                                                                                                                                                                                                                                                                  This invention relates to defence-related signalling genes isolated from CC the sunflower (Helianthus annuus). The genes encode a neoxanthin cleavage CC enzyme (NCE), an amino acid permease (AAP) and a glutamic acid rich CC protein (GRP). The signalling gene is useful for increasing the CC resistance of a plant to a pathogen such as fungus, virus, bacterium, CC nematode or insect (e.g. European corn borer), preferably CC Sclerotinia spp., Phoma spp., or Phomopsis spp. by stably incorporating a CC construct containing the gene into the genome of the plant. The gene is CC useful for regulating gene expression in a plant, in response to a cc stimulus such as infection with a pathogen, damage from a pathogen, CC hydrogen peroxide, jasmonic acid, methyl jasmonate, salicylic acid, coxalic acid or expression of a gene encoding oxalic acid oxidase. The cc a plant. The genes are useful in agriculture, particularly in the cc breeding of crop plants with improved agronomic traits, for modifying content in plants. The present sequence represents a neoxanthin cleavage enzyme-like protein from Arabidopsis thaliana, used in the characterisation of sunflower NCE.
                                                                                                                                                                                                                          Query
Best I
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated defence-related signalling gene isolated from sunflower encoding neoxanthin cleavage enzyme, amino acid permease or glutamic acid-rich protein useful for increasing resistance of plant to a
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23-MAY-2000;
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                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 1; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Defence-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neoxanthin cleavage enzyme-like protein amino acid sequence
                 221
                                           150
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                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                          Match
                 T-GIARLMLFYARAAAGIVDPAHGTGVANAGLVYFNGRLLAMSEDDLPYQVQITPNGDLK
                                                                                                                           GFLVSHEKLHPLPKTADPSVQIAGNFAPVNEQPVRRNLPVV-GKLPDSIKGVYVRNGANP 160
                                                                                                                                                      spitnpsdnndrrnkpktlh---nrtnhtlvssppklrpemtlatalf----ttvedvin 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino
                                          qflprgpyhlfdgdgmlhaikihngkatlcsryvktykynvekqtgapvmpnvfsgfngv
                                                                                                                                                                                SRVTRKLNVSSALHTPPALHFPKQSSNSPAIVVKPKAKESNTKQMNLFQRAAAAALDAAE 101
                                                                    LHEPVTGHHFFDGDGMVHAVKFEHGSASYACRFTQTNRFVQERQLGRPVFPKAIGELHGH
                                                                                                                                                                                                               210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIONEER HI-BRED INT INC. CURAGEN CORP.
                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resistance; abscisic acid metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid
                                                                                                                                                                                                                                                                                  595 AA;
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                                                                                                                                                                                                            Score 968; DB 22;
Pred. No. 8.3e-89;
6; Mismatches 220;
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                                                                                                                                                                                                             36;
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                                                                                                                                                                                                            Gaps
                                                                                               149
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AAG31334
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25-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hybridisation assay; genetic mapping;
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990S-0146388. 990S-0147038. 990S-0147038. 990S-0147704. 990S-0147720. 990S-0147720. 990S-0147720. 990S-0147749. 990S-0148341. 990S-0148341. 990S-0148341. 990S-0149722. 990S-0149929. 990S-0149929. 990S-015966. 990S-016076. 990S-016076. 990S-016081.	

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Matches 197
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25-OCT-1999
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                                                                                                        hybridisation assay; genetic mapping; termination sequence.
                                                                                                                                   Protein identification; signal transduction
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                              06-SEP-2000
                                                      EP1033405-A2
                                                                               Arabidopsis thaliana
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197; Conserv
                                                                                                                                                                                                                                          standard;
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99US-0161993.
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Pred. No. 5.4e-88;
8; Mismatches 183
                                                                                                                      gene expression
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                                                                                                                      pathway; metabolic
expression control;
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promoter;
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hes 198;
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           A DNA encoding a protein with a neoxanthin cleavage activity for producing transgenic plants with improved or decreased stress tolerance
                                       WPI; 2001-400081/43.
N-PSDB; AAD09397.
                                                                                                                                                                     Arabidopsis thaliana.
                                                                                                                                                                                             Neoxanthin cleavage enzyme; AtNCED4; abscisic acid; ABA; herbicide; stress tolerance; transgenic plant; plant breeding; antisense-therapy;
                                                                                                                                                                                                                     Arabidopsis thaliana neoxanthin cleavage enzyme, AtNCED4.
                                                                                                                                                                                                                                                                      AAE04785 standard;
                                                              Iuchi S,
                                                                              (RIKE ) RIKEN KK.
                                                                                              13-JAN-2000;
11-JAN-2001;
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Example 10; Fig 10; 101pp; English.

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CC corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key CC corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key CC role in endogenous abscisic acid (ABA) biosynthesis under drought stress. CC Neoxanthin cleavage enzyme is used for improving stress tolerance in a CC plant when expressed in a plant cell. The invention also relates to methods for increasing or decreasing stress tolerance in a plant by CC introducing the DNA into the plant, and a transgenic plant into which a CC neoxanthin cleavage enzyme is introduced. The improvement of stress CC tolerance in plants is useful, for example in plant breeding. Neoxanthin CC cleavage enzyme genes are useful for producing transgenic plants. An arid CC company the weed by growing transformant weed for several years and CC then removing the weed by growing transformant weed for several years and CC weed by inducing an inducible promoter. The present sequence is CC Arabidopsis thaliana neoxanthin cleavage enzyme, AtNCED4 protein.
CC The AtNCED4 cDNA is obtained from a Arabidopsis plant-derived cDNA CC ibbrary using a cDNA of the CPRO55 (CowPea Responsive to Dehydration) CC gene isolated from cowpea plant as a probe.
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                                                                                                                      GDNRYGGEPLFLPGEGGEEDEGYILCFVHDEKTWKSELQIVNAVSLEVE--ATVKLPSRV 580
                                                                                                                                                                            vdfprinecytgkkqryvygtildsiakvtgiikfdlhaeaetgkrmlevggnikgiydl 458
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Search completed: Job time: 45 sec

July 19, 2002, 10:11:42

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1: pir1:*
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 July 19, 2002, 10:11:03 ; Search time 21.04 Seconds (without alignments) 2735.623 Million cell updates/sec
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Copyright (c) 1993 - 2000 Comp
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358

NAWEEPETDEVVVIGSCMTPPDSIFNESDENLKSVLSEIRLNLKTGESTRRPIISNEDQQ 473

FVVVPDQQVVFKLPEMIRGGSPVVYDKNKVARFGILDKYAEDSSNIKWIDAPDCFCFHLW 413 MIAHPKLDPVSGELFALSYDVIQKPYLKYFRFSKNGEKSNDVEIPVEDPTMMHDFAITEK 357

FVIIPDQQVVFKMSEMIRGGSPVVYDKNKVSRFGILDKYAKDGSDLKWVEVPDCFCFHLW

354

294 238

MIAHPKVDPESGELFALSYDVVSKPYLKYFRFSPDGTKSPDVEIQLDQPTMMHDFAITEN 353

LFGLIDHSRGTGVANAGLYYFNNRLLAMSEDDLPYHVKVTPTGDLKTEGRFDFDGQLKST AAGIVDPAHGTGVANAGLVYFNGRLLAMSEDDLPYQVQITPNGDLKTVGRFDFDGQLEST DGMVHAVQFKNGSASYACRFTETERFVQEKALGRPVFPKAIGELHGHSGIARLMLFYARG DGMVHAVKFEHGSASYACRFTQTNRFVQERQLGRPVFPKAIGELHGHTGIARLMLFYARA PKTADPSVQIAGNFAPVNEQPVRRNLPVVGKLPDSIKGVYVRNGANPLHEPVTGHHFFDG 173 FPKQSSNYQTPKTSTISHPKQENNNSSSSISKWNLVQKAAAMALDAVEGALTKHELEHPL 117

297 293 237

178

174 118

233

177

58

FPKQSSN----SPAIVVKPKAKESNT----KQMNLFQRAAAAALDAAEGFLVSHEKLHPL 113

TTTSHATNTWI-----KPKLSMPSSKEFGFASNSISLLKNQHNRQSLNINSSLQAPPILH

57

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	
102.5	103	103	103.5	104.5	104.5	105	105.5	106	106	106.5	107	107	107.5	108	110.5	
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cell wall degrada	BIR repeat contain	phenylalaninetRN	hypothetical prote	phycobilisome link	MYC-related DNA bi	fatty-acid synthas	pristinamycin I sy	chondroitin sulfat	hypothetical prote	hypothetical prote	titin, cardiac mus	mitotic checkpoint	serine/threonine-s	conserved hypothet	protein kinase Pak	

ALIGNMENTS

probable 9-cis-epoxycarotenoid dioxygenase [imported] - potato C;Species: Solanum tuberosum (potato) C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change C;Accession: T51936 R;Burbidge, A.; Taylor, I.B.; Thompson, A. submitted to the EMBL Data Library, March 2000 A;Description: Potato putative 9-cis-epoxycarotenoid dioxygenas A;Reference number: Z25874 A;Accession: T51936 A;Accession: T51936 A;Accession: T51937 Taylor, I.B.; Tanslated from GB/EMBL/DDBJ A;Accession: T51938 A;Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residues: 1-604 <BUR> A;Cross-references: EMBL:AJ276244; PIDN:CAB76920.1 Query Match Best Local Matches S TATAAVSGRWLGGNHTQPPLSSSQSSDLSYCS---SLPMASRVTRKLNVSSALHTPPALH Similarity Conservative 72.7%; 71.3%; ; Score 2289; DB 2; ; Pred. No. 1.2e-165; 66; Mismatches 90; 20-Oct-2000 #text_change dioxygenase Length 604; Indels 18; 20-Oct-2000 Gaps 61 5.

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nine-cis-epoxycarotenoid dioxygenase - tomato
N;Alternate names: probable neoxanthin cleavage enzyme
C;Species: Lycopersicon esculentum (tomato)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #tex
C;Accession: T07123
R;Burbidge, A.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z15934
A;Accession: T07123
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A; Residues: 1-605 <BUR>
A; Cross-references: EMBL: 297215;
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GLFGLVDHSKGTGVANAGLVYFNNRLLAMSEDDLPYHVKVTPTGDLKTEGRFDFDGQLKS
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                                                   GDGMVHAVKFEHGSASYACRFTQTNRFVQERQLGRPVFPKAIGELHGHTGIARLMLFYAR 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNLEAGMVNRNMLGRKTKFAYLALAEPWPKVSGFAKVDLTTGEVKKHLYGDNRYGGEPLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATAAVSGRWLGGNHTQPPLSSSQSSDLSYCS---SLPMASRVTRKLNVSSALHTPPALH 61
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                                                                                                              NEVVIPDQQVVFKMSEMIRGGSPVVYDKNKVSRFGILDKYAKDGSDLKWVEVPDCFCFHL
                                                                                                                           NFVVVPDQQVVFKLPEMIRGGSPVVYDKNKVARFGILDKYAEDSSNIKWIDAPDCFCFHL
                                                                                                                                                                    TMIAHPKLDPVSGELFALSYDVIQKPYLKYFRFSKNGEKSNDVEIPVEDPTMMHDFAITE
                                                                                                                                                                                   TMIAHPKVDPESGELFALSYDVVSKPYLKYFRFSPDGTKSPDVEIQLDQPTMMHDFAITE
                                                                                                                                                                                                                                                                                  GDGMVHAVQFKNGSASYACRFTETERLVQEKALGRPVFPKAIGELHGHSGIARLMLFYAR
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Pred. No. 5.1
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sion 30-Apr-1999 #text_change 20-Jun-2000
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.1e-165;
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x;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; (
nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabido
A;Reference number: A66141; MUID:21016719
A;Status: preliminarry
A.M.: Presser, C.M.; Venter, J.C.; Davis, R.W.
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001
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A; Residues: 1-657 <S
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Best Local Similarity
Matches 419; Conser
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                                                                                                      QPTMIHDFAITENFVVIPDQQVVFRLPEMIRGGSPVVYDEKKKSRFGILNKNAKDASSIQ
                                                                                                                                                                                                                                                                                                                                     LHEPVTGHHFFDGDGMVHAVKFEHGSASYACRFTQTNRFVQERQLGRPVFPKAIGELHGH
                                                                                                                                                                                                                                                                                                                                                                                                        GFLVSHE-KLHPLPKTADPSVQIAGNFAPVNEQPVRRNLPVVGKLPDSIKGVYVRNGANP 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MASFTATAAVSGRWL-----GGNHTQPPLSSSQSSDLSYCSSLP------MASRVT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDLAKQ
                                                      WIDAPDCFCFHLWNAWEEPETDEVVVIGSCMTPPDSIFNESDENLKSVLSEIRLNLKTGE 460
                                                                                                                                   QPTMMHDFAITENFVVVPDQQVVFKLPEMIRGGSPVVYDKNKVARFGILDKYAEDSSNIK 400
                                                                                                                                                                                                                                                                TGIARLMLFYARAAAGIVDPAHGTGVANAGLVYFNGRLLAMSEDDLPYQVQITPNGDLKT 280
                                                                                                                                                                                                                                                                                                                                                                                      NAMISHERRRHPHPKTADPAVQIAGNFFPVPEKPVVHNLPVTGTVPECIQGVYVRNGANP
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 STRRPIISNEDQQVNLEAGMVNRNMLGRKTKFAYLALAEPWPKVSGFAKVDLTTGEVKKH
                                    WIEVPDCFCFHLWNSWEEPETDEVVVIGSCMTPPDSIFNEHDETLQSVLSEIRLNLKTGE
                                                                                                                                                                           SGRYDFDGQLKSTMIAHPKIDPETRELFALSYDVVSKPYLKYFRFTSDGEKSPDVEIPLD
                                                                                                                                                                                                                                                LGIAKLMLFNTRGLFGLVDPTGGLGVANAGLVYFNGHLLAMSEDDLPYHVKVTQTGDLET
                                                                                                                                                                                                                                                                                                                 LHKPVSGHHLFDGDGMVHAVRFDNGSVSYACRFTETNRLVQERECGRPVFPKAIGELHGH
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67.78;
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Pred. No. 1.3e-156;
80; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NID: g8052533;
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e plant Arabidopsis
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Maiti, R.; M
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Dewar,
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Marzia
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probable 9-cis-epoxycarotenoid dioxygenase [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: A86425
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Devansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; M. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
R;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; T. Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Tille: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Status: preliminary
A;Maccession: A86425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE005172; NID:g11094779; PIDN:AAG29711.1; GSPDB:GN00141 C;Genetics:
A;Map position: 1
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A; Residues: 1-589 <STO>
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Best Local S
Matches 39(
 437
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                                                                                                                                                                                                                                                                                                               LYGDNRYGGEPLFLPGEGGEEDEGYILCFVHDEKTWKSELQIVNAVSLEVEATVKLPSRV
                                                                                                                      PYQVQITPNGDLKTVGRFDFDGQLESTMIAHPKVDPESGELFALSYDVVSKPYLKYFRFS 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQSSDLSYCSSLPMASRVTRKLNVSSALHTPPALHFPKQSSNSPAIVVKPKAKESNTKQM 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYGFHGTFISKEDLSKQAL 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYGFHGTF IGADDLAKQVV
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SVLSEIRLNLKTGKSTRRTIIPG-SVQMNLEAGMVNRNLLGRKTRYAYLAIAEPWPKVSG
                                                                           GILDKYAEDSSNIKWIDAPDCFCFHLWNAWEEPETDEVVVIGSCMTPPDSIFNESDENLK 446
                                                                                                                                                                                                                                                                  NLFQRAAAAALDAAEGFLVSHEKLHPLPKTADPSVQIAGNFAPVNEQPVRRNLPVVGKLP 146
                               SVLSEIRLNLKTGESTRRPIISNEDQQVNLEAGMVNRNMLGRKTKFAYLALAEPWPKVSG
                                                           GILPRNAKDASEMVWVESPETFCFHLWNAWESPETDEVVVVIGSCMTPADSIFNECDEQLN
                                                                                                                                                                                        PYQVRVTDNGDLETIGRFDFDGQLSSAMIAHPKIDPVTKELFALSYDVVKKPYLKYFKFS
                                                                                                                                                                                                                                                   SPIFPKAIGELHGHSGIARLMLFYARGLFGLLNHKNGTGVANAGLVYFHDRLLAMSEDDL
                                                                                                                                                                                                                                                                                                                                                                               NPLQRAASAALDFAETALLRRERSKPLPKTVDPRHQISGNYAPVPEQSVKSSLSVDGKIP
                                                                                                                                                                                                                                                                                                                                                                                                                                          SPSSSVSFTNTKPR----RRKLSANSVSDTPNLLNFPNYPSPNPII-----PEKDTSRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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68.1%;
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Pred. No. 4.1e-147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.J.; Federspiel, N.A.; Kaul, S.; White, Conway, A.B.; Conway, A.R.; Creasy, T.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101;
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Maiti, R.; M
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A; Residues: 1-583 <BEV>
A; Cross-references: EMBL: AL021710
A; Cross-references: EMBL: AL021710
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R;Bevan, M.; Hilbert, H.; Braun, M.; submitted to the Protein Sequence Dai
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A; Note: F28J12.10;
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A; Residues: 1-377 <BEW>
A; Cross-references: EMB
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Best Local
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417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDSIFNESDENLKSVLSEIRLNLKTGESTRRPIISNEDQQVNLEAGMVNRNMLGRKTKFA 493
                                                                                                                                        VVSKPYLKYFRFSPDGTKSPDVEIQLDQPTMMHDFAITENFVVVPDQQVVFKLPEMIRGG
                                                                                                                                                                                                       FNGRLLAMSEDDLPYQVQITPNGDLKTVGRPDFDGQLESTMIAHPKVDPESGELFALSYD 313
                                                                                                                                                                                                                                                                                                                SVRRNLTVEGTIPDCIDGVYIRNGANPMFEPTAGHHLFDGDGMVHAVKITNGSASYACRF 176
                                                                                                                                                                                                                                                                                                                                                                                            VKPKAKESNTKQMNLFQRAAAAALDAAEGFLVSHEKLHPLPKTADPSVQIAGNFAPVNEQ 133
                                                                                                                                                                                                                                                                    TQTNREVQERQLGRPVFPKAIGELHGHTGIARLMLFYARAAAGIVDPAHGTGVANAGLVY 253
                                                                                                                                                                                                                                                                                                                                                PVRRNLPVVGKLPDSIKGVYVRNGANPLHEPVTGHHFFDGDGMVHAVKFEHGSASYACRF 193
                                                           SPVVFDGEKVSRLGIMPKDATEASQIIWVNSPETFCFHLWNAWESPETEEIVVIGSCMSP
                                                                                        SPVVYDKNKVARFGILDKYAEDSSNIKWIDAPDCFCFHLWNAWEEPETDEVVVIGSCMTP 433
                                                                                                                        VVKKPYLKYFRESPDGVKSPELEIPLETPTMIHDFAITENEVVIPDQQVVFKLGEMISGK
                                                                                                                                                                                      FNNRLLAMSEDDLPYQLKITQTGDLQTVGRYDFDGQLKSAMIAHPKLDPVTKELHALSYD
                                                                                                                                                                                                                                                  TKTERLVQEKRLGRPVFPKAIGELHGHSGIARLMLFYARGLCGLINNQNGVGVANAGLVY
                                                                                                                                                                                                                                                                                                                                                                                                                                          GGIKTWP----QAQIDLGFRPIKRQPKVIKCTVQIDVTE-LTKKRQLFTPRTTATPP---
ADSIFNERDESLRSVLSEIRINLRTRKTTRRSLLVNED--VNLEIGMVNRNRLGRKTRFA
                                                                                                                                                                                                                                                                                                                                                                          -----QHNPLRLNIFQKAAAIAIDAAERALISHEQDSPLPKTADPRVQIAGNYSPVPES 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 1991; DB 2;
; Pred. No. 4.7e-143;
82; Mismatches 105;
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Indels

22;

Gaps

6,

62

236

296

416

474

356 373

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A:Experimental source: cultivar Columbia; BAC clone F28J12 R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, submitted to the Protein Sequence Database, February 1999 A;Reference number: Z15390 A;Accession: T04937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nine-cis-epoxycarotenoid dioxygenase homolog F28U12.10 - Arabidopsis thalia
N;Alternate names: hypothetical protein T9A21.200
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   February
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E.; Brandt,
                                                                                                                                       clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1998
Length 583;
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                                                                                                                                                                                                                                                                                                  H.W.;
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A; Gene: vp14
A; Map position: 1
C; Function:
A; Description: catalyzes
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A;Residues: 1-604 <TAN>
A;Cross-references: EMBL:U95953; NID:g2232016; PIDN:AAB62181.1; PID:g2232017
A;Experimental source: strain W22
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: VP14 protein
C;Species: 2ea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision
C;Accession: T04351
R;Tan, B.C.; McCarty, D.R.
submitted to the EMBL Data Library, Mar
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A; Accession: T04351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YLALAEPWPKVSGFAKVDLTTGEVKKHLYGDNRYGGEPLFLPGEGG----EEDEGYILCF
                                            SYDVVSKPYLKYFRESPDGTKSPDVEIQLDQPTMMHDFAITENFVVVPDQQVVFKLPEMI
                                                                                                                                                                                                                                                 CRFTQTURFVQERQLGRPVFPKAIGELHGHTGIARLMLFYARAAAGIVDPAHGTGVANAG
RYAYLAVAEPWPKESGFAKEDLSTGELTKFEYGEGRFGGEPCFVPMDPAAAHPRGEDDGY
         CRFTETARLRQERAIGRPVFPKAIGELHGHSGIARLALFYARAACGLVDPSAGTGVANAG
                                                                                                                                                                                                                                                                                                 EQPVRRNLPVVGKLPDSIKGVYVRNGANPLHEPVTGHHFFDGDGMVHAVKFEHGSA-SYA 190
                                                                                                                                                                                                                                                                                                                                    AAPRKAEGGKKQLNLFQRAAAAALDAFEEGFVANVLERPHGLPSTADPAVQIAGNFAPVG
                                                                                                                                                                                                                                                                                                                                                -KPKAKESNTKQMNLFQRAAAAALDA-AEGFLVS-HEKLHPLPKTADPSVQIAGNFAPVN 131
                                                                                                                                                                                                                                                                                                                                                                                 PARSRARAS-----NSVRFSPRAVSSVPPAECLQAPFHKPVADLPAPSRKPAAIAVPGHA
                                                                                                                                                                                                                                                                                                                                                                                                        PPLSSSQSSDLSYCSSLPMASRVTRKLNVSSALHTP---PALHFPKQSSNSPAIVV----
                                                                                                                                                                                        LVYFNGRLLAMSEDDLPYHVRVADDGDLETVGRYDFDGQLGCAMIAHPKLDPATGELHAL
                                                                                                                                                                                                                                                                                     ERPPVHELPVSGRIPPFIDGVYARNGANPCFDPVAGHHLFDGDGMVHALRIRNGAAESYA
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63.3%;
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Pred. No. 2.1e:
73; Mismatches
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138;
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hypothetical protein T18B16.140 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999 C;Accession: T04438
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A; Note: T18B16.140
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A; Residues: 1-595 <BEV>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                         TASVARGALTAARVLTGQYNPVNGIGLANTSLAFFSNRLFALGESDLPYAVRLTESGDIE
                                                                                                                                                                                                                                                                                                                                                                                           T-GIARLMLFYARAAAGIVDPAHGTGVANAGLVYFNGRLLAMSEDDLFYQVQITFNGDLK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFLVSHEKLHPLPKTADPSVQIAGNFAPVNEQPVRRNLPVV-GKLPDSIKGVYVRNGANP 160
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SPELEIVAAVRLPRRVPYGFHGLFVKESDLNK
                           S--LEVEATVKLPSRVPYGFHGTFIGADDLAK 596
                                                                                                                        LVTGIVRRHPISAR-----NLDFAVINPAFLGRCSRYVYAAIGDPMPKISGVVKLDVSKG
                                                                                                                                                     LKTGESTRRPIISNEDQQVNLEAGMVNRNMLGRKTKFAYLALAEPWPKVSGFAKVDLTTG
                                                                                                                                                                                                                                                                                                              TIGRYDFDGKLAMSMTAHPKTDPITGETFAFRYGPV-PPFLTYFRFDSAGKKQRDVPIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                     QFLPRGPYHLFDGDGMLHAIKIHNGKATLCSRYVKTYKYNVEKQTGAPVMPNVFSGFNGV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LHEPVTGHHFFDGDGMVHAVKFEHGSASYACRFTQTNRFVQERQLGRPVFPKAIGELHGH 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFIDP-----PSRPSVDPKHVLSDNFAPVLDELPPTDCEIIHGTLPLSLNGAYIRNGPNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPITNPSDNNDRRNKPKTLH----NRTNHTLVSSPPKLRPEMTLATALF----TTVEDVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210;
                                                           DRDDCTVARRMYGSGCYGGEPFFVARDPGNPEAEEDDGYVVTYVHDEVTGESKFLVMDAK
                                                                                      E-----VKKHLYGDNRYGGEPLFLPGEGG----EEDEGYILCFVHDEKTWKSELQIVNAV 566
                                                                                                                                                                                   ESEMKWFEVPGFNIIHAINAWDEDDGNSVVLIAPNIMSIEHTLERMD-LVHALVEKVKID
                                                                                                                                                                                                                  SSNIKWIDAPDCFCFHLWNAWEEPETDEVVVIGSCMTPPDSIFNESDENLKSVLSEIRLN 455
                                                                                                                                                                                                                                               MTSPSFLHDFAITKRHAIFAEIQLGMRMNMLDLVLEGGSPVGTDNGKTPRLGVIPKYAGD
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Pred. No. 2.3e-65;
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Database,
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594
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April 1998
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RESULT T49193

neoxanthin

cleavage e names: p

protein

ncl - Arabidopsis MAA21.150

thaliana

N; Alternate

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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49193
R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemc submitted to the Protein Sequence Database, April 2000
A;Reference number: 225018
A;Accession: T49193
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-538 <AIE>
A;Cross-references: EMBL:AL163818; GSPDB:GN00061; ATSP:MAA21.150
A;Experimental source: cultivar Columbia; BAC clone MAA21
C;Genetics:
A;Gene: ATSP:MAA21.150
A;Map position: 3
A;Introns: 72/3; 96/2; 101/2; 138/3; 172/1; 193/1; 230/1; 291/3; 338/1; 377/2; 411/
RESULT
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                                                                                                                                                                                   PYGFHALFVTEEQLQEQTL
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                                                                                                                                                                                                                 PYGFHGTFIGADDLAKQVV
                                                                                                                                                                                                                                               GEGRYGSEAIYVPRETAEEDDGYLIFFVHDENTGKSCVTVIDAKTMSAEPVAVVELPHRV
                                                                                                                                                                                                                                                                        GDNRYGGEPLFLPGEGGEEDEGYILCFVHDEKTWKSELQIVNAVSLEVE--ATVKLPSRV
                                                                                                                                                                                                                                                                                                       VDFPRINECYTGKKQRYVYGTILDSIAKVTGIIKFDLHAEAETGKRMLEVGGNIKGIYDL
                                                                                                                                                                                                                                                                                                                                   LEAGMVNRNMLGRKTKFAYLALAEPWPKVSGFAKVD------LTTGEVKKHLY--
                                                                                                                                                                                                                                                                                                                                                                                                                             MHFRPKEMVKEKKMIYSFDPTKKARFGVLPRYAKDELMIRWFELPNCFIFHNANAWE--E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGNGTANTALVYHHGKLLALQEADKPYVIKVLEDGDLQTLGIIDYDKRLTHSFTAHPKVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGTGVANAGLVYFNGRLLAMSEDDLPYQVQITPNGDLKTVGRFDFDGQLESTMIAHPKVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEHGSASYACRFTQTNRFVQERQLGRPVFPKAIGELHGHTGIARLMLFYARAAAGIVDPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLSDGSSIISVHPRPSKGFSSKLLDLLERLVVKLM------HDASLPLH-----Y
                                                                                                                                                                                                                                                                                                                                                                   EDEVVLITCRLENPDLDMVSGKVKEKLENFGNELYEMRFNMKTGSASQKKLSASA-----
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207; Conserv
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               Arabidopsis
                                                                           #text_change
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A;Status: preliminary; translated from A;Molecule type: mRNA
A;Residues: 1-538 <NEI>
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Best Local S
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                      PYGFHGTFIGADDLAKQVV
                                                                           GDNRYGGEPLFLPGEGGEEDEGYILCFVHDEKTWKSELQIVNAVSLEVE--ATVKLPSRV
                                                                                                                                                                                                 TDEVVVIGSCMTPPD-----SIFNESDENLKSVLSEIRLNLKTGESTRRPIISNEDQQVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLSDGSIIISVHPRPSKGFSSKLLDLLERLVVKLM------
PYGFHALFVTEEQLQEQTL
                                                            GEGRYGSEAIYVPRETAEEDDGYLIFFVHDENTGKSCVTVIDAKTMSAEPVAVVELPHRV
                                                                                                                                           LEAGMYNRNMLGRKTKFAYLALAEPWPKVSGFAKVD------LTTGEVKKHLY--
                                                                                                                                                                                 EDEVVLITCRLENPDLDMVSGKVKEKLENFGNELYEMRFNMKTGSASQKKLSASA-----
                                                                                                                                                                                                                                           MHFRPKEMYKEKKMIYSFDPTKKARFGYLPRYAKDELMIRWFELPNCFIFHNANAWE--E
                                                                                                                                                                                                                                                                      VVFKLPEMIRGGSPVV-YDKNKVARFGILDKYAEDSSNIKWIDAPDCFCFHLWNAWEEPE
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                                                                                                                                                                                                                                                                                                                                                                                                                             IKDGKATYVSRYVKTSRLKQEEFFGAAKFMK-IGDLKGFFGLLMVNIQQLRTKLKILDNT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSGNFAPIRDETPPVKDLPVHGFLPECLNGEFVRVGPNPKFDAVAGYHWFDGDGMIHGVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KQSSNSPAIVVKPK-AKESNTKQMNLFQRAAAAALDAAEGFLVSHEKLHPLPKTADPSVQ 122
                                                                                                                      VDFPRINECYTGKKQRYVYGTILDSIAKVTGIIKFDLHAEAETGKRMLEVGGNIKGIYDL
                                                                                                                                                                                                                                                                                                         PVTGEMFTFGYS-HTPPYLTYRVISKDGIMHDPVPITISEPIMMHDFAITETYAIFMDLP
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37.0%;
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C; Accession: AG1944
R; Kaneko, T.; Nakamura, Y.;
Nakazaki, N.; Shimpo, S.; S
DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic So
A; Molecule type: DNA
A; Residues: 1.475 <KUR>
A; Cross-references: GB:BA000019;
A; Experimental source: strain PCC
                                                                                                       A; Reference number: AB1807; A; Accession: AG1944
                                                                                                                                                                                                                                                   A; Note: Anabaena sp. (strain PCC 7120)
C; Date: 14-Dec-2001 #sequence_revision
                                                                                                                                                                                                                                                                                             hypothetical protein all1106 [imported] - C; Species: Anabaena sp.
                                                                               A; Status: preliminary
                                                                                                                               Sequence of the Filamentous Nitrogen-fixing 7; MUID:21595285; PMID:11759840
                                                                                                                                                                                        : Wolk, C.P.; P
Sugimoto, M.;
    DOG
PIDN:BAB73063.1;
C 7120
                                                                                                                                                                                                                                                        is a synonym of Nostoc sp. strain PC 14-Dec-2001 #text_change 11-Jan-2002
                                                                                                                                                                                          Kuritz, T.; Sas
; Takazawa, M.;
                                                                                                                                                                                                                                                                                                                   Anabaena sp.
                                                                                                                                                                                                                T.; Sasamoto,
                     PID:g17130452;
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                                                                                                                                                                                          S.; Watanabe,
, M.; Yasuda,
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                        GSPDB:GN00179
                                                                                                                                                Cyanobacterium
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PCC

7120

X : Α:,

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hypothetical protein - apple tree
C;Species: Malus domestica (apple tree)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C;Accession: T17019
C;Accession: T7019
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T17019
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                                                                                                                                                                                                                                                A;Title: Apple messenger RNAs related to bacterial A;Reference number: 218655; MUID:98179104 A;Accession: T17019
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                                                                                                                                                                      A;Cross-references: EMBL:293765; NID:g2924324; PIDN:CAB07784.1; PID:g2924325 A;Experimental source: cv. McIntosh, strain Wijcik
                                                                                                                                                                                                                                                                                             R; Watillon, B.; Kettmann, R.; Arredouani, A.; Hecquet, J.; Plant Mol. Biol. 36, 909-915, 1998
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A; Gene: all1106
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nes 169; Conservative
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                             ESTMIAHPKVDPESGELFALSYDVVSKPYLKYFRFSPDGTKSPDVEI-QLDQPTMMHDFA
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--DDVASEFPRINENFLGQPTQYGYTSRLAKGSTPLFEGLIKYDLSNAKSQNYEYGQGRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---PAHGTGVANAGLVYFNGRLLAMSEDDLPYQVQITPNGDLKTVGRFDFDGQLESTMIA
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                                                                                                          Similarity
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                                                                                                          23.7%;
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; Pred. No. 1.3e-48;
91; Mismatches 171;
                                                                                            Score 745; DB 2;
Pred. No. 1.3e-48;
6; Mismatches 129
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C;Genetics:
A;Gene: CC0776
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87345
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C;Accession: E87345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein CC0776 [imported] - Caulobacter crescentus C_iSpecies: Caulobacter crescentus
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A; Residues: 1-483 <STO>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ERLPPVRTSLGPTNHPYMTGPWTPQHEEVNAWDLEVLEGAIPADLDGVYLRNTENPVHDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160;
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LKSVLSEI----RLNLKTGESTRRPIISNEDQQVNLEAGMVNRNMLGRKTKFAYLALAEP-
                                       GEPRWFEAEPTYVLHWLNAYE--DGDEVVLDGYFQEKPIPRPLEGAPDGHGHLMAYLDEH
                                                                            SNIKWIDAPDCFCFHLWNAWEEPETDEVVVIGSCMTPP---
                                                                                                                     VPLPGPRLPHDMAFSSKYAILNDLPVFWDQELMARDIHAVRLHKGIPSRFALVPR---EG
                                                                                                                                                          IQLDQPTMMHDFAITENFVVVPDQQVVFKLPEMIRGGSPVVYDKNKVARFGILDKYAEDS
                                                                                                                                                                                                 ENLGVASW-APLEG-VSAHPKVDEATGELMFFNY---SKAWPYMHYGVVGPDGKRKVYQG
                                                                                                                                                                                                                                                                              K-----RPGFG----AHGALKDSASTDIVVHNGEAIATF----YQCGEAYRLDPL-TL
                                                                                                                                                                                                                                                                                                                                                          IGRYHPFDGDGMIHQIEFKGGAATYRNRFVRTRCFEAEQEVNEGLW----GGLMDGPGVS
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A;Gene:
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A; Accession: A70534
A; Status: preliminar; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-501 <COL>
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  GE-EDEGYILCEVHDEKTWKSELQIVNAVSLEVEATVKLPSRVPYGFHGTF
                                                                                                                                                                                                                                                                   AWNPSYPARVGVMPREG-GNEDVRWFDIEPCYVYHPLNAYSECRNGAEVLVLDVVRYSRM
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                                                                                                                                                                                                    TPPDSIFNESDENLKSVLSEIRLNLKTGESTRRPIISNEDQQVNLEAGMVNRNMLGRKTK
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                                                                                                                                                                                                                                                                                                                  VYDKNKVARFGILDKYAEDSSNIKWIDAPDCFCFHLWNAWEEPETD-EVVVIG----
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                                                                        FAYTVGIEGGFLVGAGAALSTP-----LYKQDCVTGSSTVASLDPDLLIGEMVFVPNPS
                                                                                                                                                                        FDRDRRGPGGDS - - RPSLDRWT INLATGAVTAE - - - CRDDRA - - QEFPRINETLVGGPHR
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27.9%;
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H37Rv
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Pred. No. 2.3e-27;
6; Mismatches 195
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hypothetical protein - Synechocystis c;Species: Synechocystis sp. A;Variety: PCC 6803 C;Date: 25-Apr-1997 *sequence_revisio
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A;Cross-references: GB:Z95210; GB:AL123456; NID:g3261757; A;Experimental source: strain H37Rv C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; A;Title: Deciphering the biology of Mycobacterium A;Reference number: A70500; MUID:98295987
A;Accession: A70582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-502 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 17-Jul-1998 #sequence_revision C;Accession: A70582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein Rv0913c - Mycobacterium C; Species: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Cole, S.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Connor, R.; Davies, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rv0913c
                                             --LPSRVPYGFHGTFIGADDLAK 596
                                                                                                                                                                                                                                                                                                                                                               TDEVVVIGSCMTPPDSIFNESD----------ENLKSVLSEIRLNLKTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QERQLGRPVFPKAIGELHGHTGIARLMLFYAR----AAAGIVDPAHGTGV-ANAGLV---
LALPERISSGTHSAWVPGAELRR
                                                                                                                                                    VKKHLYGDNRYGGEPLFLPGEGGE-EDEGYILCFVHDEKTWKSELQIVNAVSLEVEATVK
                                                                                                                                                                                                                                                        STRRPIISNEDQQVN---LEAGMVNRNMLGRKTKFAYLALAEP-WPKVSGFAKVDLTTGE
                                                                                                                                                                                                                                                                                                              GDEIVLDG------FYEGDPQPLDTGGTKWEKLFRFLALDRLQSRLHRWRLNMVTG-
                                                                                                                                                                                                                                                                                                                                                                                                                  --FPLFWDPRLLERDVHLPRFYPEIPSRFAVVARRGNDIRWFEADPTFVLHFTNAYE--Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGSPVVYDKNKVARFGILDKY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YDVVSKPYLKYFRFSPDGTKSPDVEIQLDQPTMMHDFAITENFVVVPDQQVVFKLPEMIR | :||::| | :|| | |||:|::|
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                                                                                                      HECYSFGDGVYGSETAMAPRVGSSAEDDGYLVTLTTDMNDDASYCLVFDAARPGDGPICK
                                                                                                                                                                                                        ----AVHEEQLSESITEFGTINADYAASSYRYTYAATGKPSWFLFDGLVKHDLLTGN
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27.6%;
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Pred. No. 1.7e-26;
489
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#sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

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A; Reference number: S74322; MUID:97061201
A; Accession: S76169
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-490 <KAN>
A; Rosidues: 1-490 <KAN>
A; Rosidues: 1-490 <KAN>
A; Rosidues: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
Search completed: July 19, Job time: 67 sec
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                                                                                                                                                                                                                                                             SICYNSLPQV--DTDGDFRSTNFD---NLDPGQLWRFTIDPAAATVEKQLMVSRCCEFPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGEGG-EEDEGYILCFVHDEKTWKSELQIVNA--VSLEVEATVKLPSRVPYGFHGTF 588
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                                                                                                   PRPGGVAEDDGWLLCLIYKADLHRSELVILDAQDITAPAIATLKLKHHIPYPLHGSW 487
                                                                                                                                                                                   VHPQQVGRPYRYVYMGAAHHSTGNAP----LQAILKVDLESGTETLRSFAPHGFAGEPIFV
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                   2002, 10:12:10
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Minimum DB
Maximum DB
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Listing first 45 summaries
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Perfect score:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ALIGNMENTS

RESULT 1 YCSO_YEAST

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                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                   FUNCTION: PLAYS AN IMPORTANT ROLE IN THE INITIATION AND REGULATION OF CHROMOSOMAL REPLICATION. BINDS TO THE ORIGIN OF REPLICATION; IT BINDS SPECIFICALLY DOUBLE-STRANDED DNA AT A 9 BP CONSENSUS (DNAA BOX): 5'-TTATC(C/A)A(C/A)A-3'. DNAA BINDS TO ATP AND TO
                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE DNAA FAMILY.
                                                                                                                                                                                                                                                                           ACIDIC PHOSPHOLIPIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVITKE---TISETDNAALPHSGSGSGITLTCQELDE----NNPFGGE
                                                                                                                                                                                                                                                                                                                                                93:27-34(1990).
                                                                                                  JQ0733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRKTKFAYLALAE----PWPKVSGFAKVDLTTGEVKKHLYGDNRYGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FNESDENLKSVLSEIRLNLKTGEST-----RRPII---SNEDQQV---NLEAGMVNRNML
                                                                                                                                                                                                                                                                                                                                                                                           eotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNIDGANATSALSKPQGSFSKEKKRITWRFKEPVVLTRNGEGQRLIARFITDGLAHESAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPDVEIQLDQPTMMHDFAITENFV--VVPDQQVVFKLPEMIRGGSPVVYDKNKVARFGIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NASFK-----DGMLQNSQLI------GEI-ALNYLPNSVMNSPL------PIG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGDLKTVGRFDFDGQLESTMIAHPKVDPESGELFALSY - - - DVVSKPYLKYFRFSPDGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELHGHTGIARLMLFYARAAAGIVDP-AHGTGVANAGLVYFNGRLLAMSEDDLPYQVQITP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---INLRINNGAKFEKVILNQAFIERVAPEE---FKV-----NPSFIDSRTLGAI---
                                                                      PF00308; bac_dnaA;
                                                                                                                                                                                                                                                                                                                                                                         otide sequence of a Proteus mirabilis DNA 60K-rnpA-rpmH-dnaA-dnaN-recF-gyrB region
                                         PR00051; DNAA.
; PS01008; DNAA; 1
                                                                                                                                            s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                   IPR001957; Bac_DnaA.
 466
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(Rel. 19, Last sequence update)
(Rel. 40, Last annotation updat
replication initiator protein d
                                                                                                     IQEBV
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AA,
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MW;
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 F8B67C142FE9FA41
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              (POTENTIAL)
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CRC64;
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Best Local 9
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                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-96112805; PubMed-8846783;
Ottille S., Miller P.J., Johnson D.I., Creasy
Bagrodia S., Forsburg S.L., Chernoff J.;
                                                                                                                                                                                                                                                                                                                                    Serine/threonine-protein kinase pakl/shkl (EC PAK1 OR SHK1 OR ORB2 OR SPBC1604.14C.
                                                                                             Beck
                                                                                                                                                       SEQUENCE FROM Marcus S.;
                                                                                                                                                                                       "Fission yeast pak1+ encodes a protein kinase Cdc42p and is involved in the control of cell EMBO\ J.\ 14:5908-5919(1995).
                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes.
                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
30-MAY-2000 (Rel. 39, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
                                                                                                        STRAIN=972;
                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                    NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                Schizosaccharomyces.
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                                                                                                                                           Submitted (APR-1997)
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                                                                              , Reinhardt R.
ed (DEC-1998)
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                                                                                 M., Rajandream M.
EMBL/GenBank/DDBJ
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Pred. No. 0.
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                                                                                                                                                                                                                                     C.L.,
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Wigler "Shk1,

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Saccharomyces

cerevisiae of a

Ste20

and mammalian

Ras/Cdc42 signaling

Marcus

Polverino

PubMed=7597098; ino A., Chang E.,

Robbins

D.,

Cobb M.H.,

SEQUENCE OF 119-658 FROM N.A. MEDLINE=95320235; PubMed=7597

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Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphorylation.

B5
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CONFLICT
SEQUENCE
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SMART; SM00220; S_TKC; 1.

PROSITE; PS50108; GB; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1

PROSITE; PS50011; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPRO02290;
InterPro; IPRO01245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            module
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                                                                                                                                                                                                                                                                                                                                                                                18 NHTQPPLSSSQSSDL------SYCSSLPMASRVTRKLNVSSALHTPPALHFPKQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
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DTFFYKSELWMVMEYMRGGSLTEVVTNNTL--SEGQIAAICKETLEGLQHLHENGIVHRD
                                     --LFYARAAAGIVDPAHGTG----VANAGLVYFNGRLLAMSEDDLPYQVQITPNG----D
                                                                                                                         HAVKFEHGSAS -- YACRFTQTNRFVQERQLGRPVFPK -- - AIGEL -- -- HGHTGIARLM
                                                                                                                                                                   ATPQKVEAPSAPRLQKRAPRQ-----QSNDSAVLAKLQSICNPKNPTLLYRNF
                                                                                                                                                                                                           DPSVQIAGNFAPVNEQPVRRNLPVVGKLPDSIKGVYVRNGANPLHEPVTGHHFFDGDGMV
                                                                                                                                                                                                                                                     NIIRSHSPVLLTPQTLSTSETKHIRPNNSTPYQRRAETSTK---
                                                                                                                                                                                                                                                                                               N-----SPAIVVKPKAKESNTKQM-----NLFQRAAAAALDAAEGFLVSHEKLHPLPKTA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L41552; AAB52609.1;
P00518; 1PHK.
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88; Conser
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PAK_box_P21_Rho_bindng.
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
GIQH -> LYSD (IN REF.
R -> P (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .'
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 107.5;
Pred. No. 2.4;
51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-SER.
POLY-SER.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> P (IN REF. 1)
69D72E5C925021E5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> LYSD (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DВ
                                                                                                                                                                                                                                                                                                                                                                                                                          157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ЬY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONTROL C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                          121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                     -PKAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          outstation
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF
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                                                                                                                                                                                                                                                     341
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RESULT 4
PGCV_CHICK
Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crbsc.

Chicken).

Gallus gallus (Chicken).

Gallus yota; Metazoa; Chordata; Craniata; Vertebrata; Euter

Eukaryota; Metazoa; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGCV
                                                                                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shinomura T., Nishida Y., Ito K., Kimata K.; "cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during chondrogenesis in chick limb buds. Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, 01-NOV-1997 (Rel. 35, 16-OCT-2001 (Rel. 40, World of the control of the co
                                                                                                                                                                                         EMBL; X60226; CAA42787.1;
EMBL; D13542; BAA02742.1;
HSSP; P20693; 1HLJ.
                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spliced multiforms of PG-M and their relationships J. Biol. Chem. 268:14461-14469(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93300846; PubMed=8314802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Versican core protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q90953; Q90945;
01-NOV-1997 (Re
                                                                                                                                                                                                                                                                                                                   entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Chondroitin
                                                                                                                                                                       [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (By similarity).

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V SIMILARITY: CONTAINS 2 LINK DOMAINS.

SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS: At least 2 isoform V1; are produced by alternative splicing TISSUE SPECIFICITY: Prechondrogenic cond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Secreted; extracellular ALTERNATIVE PRODUCTS: At least 2 isoforms; VO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JIOL. Chem. 268:14461-14469(1993).
FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part connecting cells with the extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               developing limb buds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEVELOPMENTAL STAGE: Disappears after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hyaluronic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVNPKQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGIMAIEMVEGEPPYLNENPLRALYLIATIGTP-----KISRPELLSSVFHDF-LSKSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IKSDNILLSLQGDIKLTDFGFCAQIDSNMTKRTTMVGTPYWMAPEVVTRKEYGFKVDVWS
                                                                                                                                                                                                                                                                                         an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                   Swiss Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEGHORN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sulfate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---VGRFDFDGQLES----TMIAHP--
                                                                                      Asx_hydroxyl.
EGF-like.
EGF_2.
EGF_Ca.
                                                                                                                                                                                                                                                                                                                   license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
precursor (Large fibroblast
proteoglycan core protein 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Limb bud;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                 copyright. It is produced through a collaboration tute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -YFRFSPDGTKSPDVEIQLDQPTMM---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   condensation
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                                                                                                                                                                                                                                                                                                                   http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                       Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cartilage development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V-TYPE
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(PG-M).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             matrix
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   area
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                                                                                                                                                                                                                                                                                                                                               commercial
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InterPro;
InterPro;

[nterPro; InterPro; InterPro; [nterPro;

IPR000742; IPR001881; IPR003599; IPR003006; IPR000538; IPR000436;

Ig_MHC.

Sushi_SCR_CCP

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PROSITE; PS00022; EGF_1; 2.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS01241; LINK; 2.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00641; C_TYPE_LECTIN_2; 1.
Glycoprotein; Proteoglycan; Lectin; Exsignal; Repeat; EGF-like domain; Calci
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SM00034; CLECT; 1.

SM00179; EGF_CA; 1.

SM00001; EGF_like; 1.

SM00409; IG; 1.
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PF00047;
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F00193; Xlink; 2.
PD000918; Link; 2.
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  lectin_c.
                    VERSICAN CORE PROTEIN.

IG-LIKE V-TYPE DOMAIN.

LINK 1.

EGF-LIKE 1.

EGF-LIKE 2, CALCIUM-BIN
C-TYPE LECTIN.

SUSHI.

BY SIMILARITY.
BY SIMIL
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Best Local
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MOUSE CAD5_MOUSE STANDARD; PRT; 783 AA.

P55284; 035542;
01-CCT-1996 (Rel. 34, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Vascular endothelial-cadherin precursor (VE-cadherin)
           STRAIN-BALB/C; TISS
MEDLINE-97364256; I
Matsuyoshi N., Toda
Takeichi M., Imamur
                                                           Blood 87:
[2]
SEQUENCE
                                                                                    Breier G., Breviario F., Caveda L., Berthier R., Schnigotsch U., Vestweber D., Risau W., Dejana E.;
"Molecular cloning and expression of murine vascular cadherin in early stage development of cardiovascular Blood 87:630-641(1996).
                                                                                                                                                                                                                   Eukaryota;
Mammalia; E
                                                                                                                                                                                                                                                        CDH5.
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MEDLINE-96141083; PubMed-8555485;
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                                                                                                                                                                                                               musculus (Mouse).
aryota; Metazoa; Chordata;
malia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                            LLITNESSGDGS--TESDLS-RSVFTEI-LTMSSHEDSEK 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MASFTATA-AVSGRWLGGNHTQPPLSSSQSSDLSYCSSLPMASRVTRKLNVSSALHT---
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M., Imamura S.;
evidence of the
                                                             FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                            N.A.
                       56; PubMed=9220534;
Toda K.-I., Horigu
                                                  TISSUE=Breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                             AND FUNCTION
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22.7%;
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 critical
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                         Horiguchi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                  carcinoma;
                                                                                                                                                                                                                  Craniata; Vertebrata;
Sciurognathi; Muridae
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 role
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No.
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 of cadherin-5
                         Tanaka
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                                                                                                                                                                                                                                                                                                                                                                                                                      464
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                         Nakagawa
 in murine
                                                                                                               endothelial-
                                                                                                                                                                                                                  Murinae;
                                                                                                  system.";
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CARBOHYD
CONFLICT
SEQUENCE
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CARBOHYD
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
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SIGNAL
PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VASCULAR INTEGRITY.";
PROC. ASSOC. AM. Physicians 109:362-371(1997).
-!- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS
-!- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS
THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
SORTING OF HETEROGENEOUS CELL TYPES. THIS CADHERIN MAY PLAY A
IMPORTANT ROLE IN ENDOTHELIAL CELL BIOLOGY THROUGH CONTROL OF THE
COHESION AND ORGANIZATION OF THE INTERCELLULAR JUNCTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00232; CADHERIN_1; 3. PROSITE; PS50268; CADHERIN_2; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00028; cadherin; 5.
Pfam; PF01049; Cadherin_C_term;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002126; Cadherin_C_term.
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217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adhesion;
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QAEYKIVVETQDALG-LRGESGTATVMI----
                                      QLGRPVFPK---
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                                                                            AVDADDPTVAGHATVLYQIVKGNEYFSIDNSGLI---
                                                                                                                                                     EYFLTALIVDKNTNKNLEQPSSFTVKVHDINDNWPVFSHQVFNASVPEMSAIGTSVIRVT
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SM00112; CA;
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                                                                                                                                                                                                                                                                                                                               Similarity
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45
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87847
                                    -AIGELHGHTGIARLMLFYARAAAGIVDPAHGTGVANAGLVYFNGRLLA
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                                                                                                                                                                                                                                                                                                                           3.3%;
                                                                                                             LHEPVTGHHFF---DGDGMVHAVKFEHGSASYACRFTQTNRFVQER
                                                                                                                                                                                                                                                                                                             101;
                                                                                                                                                                                                                                                                                                                                                                                                            ¥.
                                                                                                                                                                                                                                                                                                         Score 105; DB Pred. No. 4.7; 01; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
CYTOPLASMIC
CADHERIN 1.
CADHERIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                             CADHERIN 3
CADHERIN 5
CADHERIN 5
SER-RICH.
N-LINKED (
N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
VASCULAR ENDOTHELIAL-CADHERIN
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                          KDQ -> GKIK (IN REF
240AF2D663BCE71C (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                          IAGNFAPVNEQPVRRNLPVVGKLPDSIKGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC.)
(GLCNAC.)
(GLCNAC.)
(GLCNAC.)
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                                                                                                                                                                                                                                                                                                             242;
                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Calcium-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                Length 783;
                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                          FTKIKNLDREK
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                                                                                                                                                                                                                                                                                                             254;
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MBL outstation -
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                                                                                                                                                                                                                                                                     112
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RESULT 6
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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fatty acid synthase (EC 2.3.1.85) [Includes: JEC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.
                 "Fatty acid synthesis: a potential selective antineoplastic therapy.";
Proc. Natl. Acad. Sci. U.S.A. 91:6379-6383(1-1-FUNCTION: FATTY ACID SYNTHETASE CATALYZE LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, THIS MULTIFUNCTIONAL PROTEIN HAS 7 CATAL ACYL CARRIER PROTEIN.
                                                                                                                                                                                                            (2)
SEQUENCE OF 753-758 AND 1285-1297.
MEDLINE-94294385; PubMed-8022791;
Kuhaida F.P., Jenner K., Wood F.D.,
                                                                                                                                                                                       MEDLINE=94294385; PubMed=80
Kuhajda F.P., Jenner K., Wo
Dick J.D., Pasternack G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAS_HUMAN
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                                                                                                                                                                                                                                                                                            Proc. Natl.
[2]
                                                                                                                                                                                                                                                                                                         MEDLINE=96004605; PubMed=7567999;
Jayakumar A., Tai M.-H., Huang W.-Y.,
Abu-Elheiga L., Chirala S.S., Wakil S.
"Human fatty acid synthase: properties
Proc. Natl. Acad. Sci. U.S.A. 92:8695-
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FASN OR FAS
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  CATALYTIC
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  ACTIVITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Primates;
Acetyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----FNESDENLKSVLSEIRLNLKTGESTRRPIISNEDQQ 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -FKLPEMIRG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GTKSPDVE----
                                                                                                                                                                                                                                                                                                                                     properties and molecular
                                                                                                                   91:6379-6383(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                92:8695-8699(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
+ N malonyl-CoA
                                                                                                                                                                   selective
                                          CATALYZES THE FORMATION TYL-COA, MALONYL-COA AND S 7 CATALYTIC ACTIVITIES
                                                                                                                                                                                                              Hennigar
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                                                                                                                                                                                                                                                                                                                                                              Al-Feel
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EC 3.
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NADPH.
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Query Match
Best Local Similarity
  Matches
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InterPro; IPR002085; Adh_zn_family.
InterPro; IPR002085; Adh_zn_family.
InterPro; IPR003880; Phosphopant_attach.
InterPro; IPR003880; Phosphopant_attach.
InterPro; IPR000051; SAM_bind.
InterPro; IPR001031; Thioesterase.
IPR001031; Thioesterase.
IPR001031; Thioesterase.
IPfam; PP00107; adh_zinc; 1.
IPfam; PF00107; adh_zinc; 1.
IPfam; PF00109; ketoacyl-synt; 1.
IPfam; PF002801; ketoacyl-synt; 1.
IPfam; PF00550; pp-binding; 1.
IPfam; PF00550; Thioesterase; 1.
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                  ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                          ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [acyl-carrier protein].

CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.

CATALYTIC ACTIVITY: (3R)-3-hydroxypalmitoyl-[acyl-carrier protein]
= 2-hexadecenoyl-[acyl-carrier protein] + H(2)0.

CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NADP(+) = trans-
2,3-dehydroacyl-[acyl-carrier protein] + NADPH.

CATALYTIC ACTIVITY: Oleoyl-[acyl-carrier protein] + H(2)0 = [acyl-carrier protein] + Madelling | Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acetyl-[acyl-carrier protein]
CATALYTIC ACTIVITY: Malonyl-CoA + [acyl-carrier
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CATALITIC ACTIVITY: Acetyl-CoA + [acyl-carrier protein] = COA +
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                                                                                                 THIOESTERASE (BY SIMILARITY).
THIOESTERASE (BY SIMILARITY).
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ACYL AND MALONYL TRANSFERASES
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SÜBUNIT: PHYCOBILISOMES OF THIS ORGANISM ARE COMPOSED OF A TWO CYLINDER CORE, FROM WHICH SIX RODS RADIACE. THE CORE IS MAINLY COMPOSED OF ALLOPHYCOCYANIN ALPHA AND BETA CHAINS, AND OF THREE MINOR COMPONENTS: THE ALLOPHYCOCYANIN ALPHA-B CHAIN, A 18.3 kDaPOLYPEPTIDE, AND THE ANCHOR POLYPEPTIDE LCM. SUBCELLULAR LOCATION: ANCHORS THE PHYCOBILISOME PERPENDICULARLY TO THE STROMAL SURFACE OF THE THYLAKOID MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: THE REPEATED DOMAINS ARE SIMILAR TO THE N-TERMINAL REGIONS OF PHYCOCYANIN ROD LINKER POLYPEPTIDES.
SIMILARITY: THE PHYCOBILIN-LIKE DOMAINS ARE SIMILAR TO PHYCOBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C. Natl. Acad. Sci. U.S.A. 87:2152-2156(1990).
FUNCTION: THIS PROTEIN IS POSTULATED TO ACT BOTH AS TERMINAL ENERGY ACCEPTOR (BY ITS PHYCOBILIN-LIKE DOMAINS) AND AS A LIP POLYPEPTIDE (BY ITS REPEATS AND ARMS) THAT STABILIZES THE PHYCOBILISOME CORE ARCHITECTURE.
                                                                                                                                                                                                                                                                                                                                             FROM VARIOUS SPECIES.
                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produ
sen the Swiss Institute of Bioinformatics
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                                                                                                                           and this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).
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R Pfam; PF00502; Phycobilisome; 2.
Phycobilisome; Electron transcriptors
                                                                  MEDIINE-98196666; PubMed-9537320; Deckert G., Warren P.V., Gaasterland T., Young W.G., Deckert G., Warren P.V., Gasterland T., Young W.G., Graham D.E., Overbeek R., Snead M.A., Keller M., Auja Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacter:
                                                                                                                                                                                                                                                                                        SYFB_AQUAE STANDARD; PRT; 775 AA. 067620; 067620; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Phenylalanyl-trNA synthetase beta chain (EC 6. TRNA ligase beta chain) (PheRS). PHET OR AQ_1730.
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CATALYTIC ACTIVITY: ATP + L-phenylalanine diphosphate + L-phenylalanyl-tRNA(Phe).
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Aminoacyl-tRNA synthetase;
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                                                                                                                                                                                                                                                                                                                                                                  --- RGVV
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Pfam; PF00211; guanylate_cyc; 1.
Pfam; PF00560; LRR; 18.
Pfam; PF00481; PP2C; 1.
SMART; SM00044; CYCC; 1.
SMART; SM00370; LRR; 6.
SMART; SM00370; LRR, TYP; 2.
SMART; SM00332; PP2CC; 1.
SMART; SM00314; RA; 1.
SMART; SM00314; RA; 1.
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Ustilago maydis (:
Eukaryota; Fungi;
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                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a coefficient the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ustilaginomycetidae;
NCBI_TaxID=5270;
                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                  EMBL; L33918; AAA57469.1;
                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95087882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adenylate
                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                  InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "cAMP regulates morphogenesis in the
                                                                                                                                                                                                                                                                                          [nterPro;
                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosy SIMILARITY: BELONGS TO ADENUTYL CYCLASE CLASS-3 FAM. SIMILARITY: COUTAINS 21 LEDICIDE-RICH REPEATS (LRR). SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        METABOLISM
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                                                                                                                                                                                                    Repeat;
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                                                                                                                                                                                                                                                                                                                 IPR001054; Guanylt_cyclase. IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cyclase
                                                                                                                                                                                                                                                                                         IPR003591; LRR_typ.
IPR001932; PP2C_domain.
                                                                                                                                                                                                                                                                                                          IPR003592; LRR_out.
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M BY CATALYSING T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smut fungus).
Basidiomycota; Ust
ae; Ustilaginales;
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OEC
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      LRR 21.
PP2C-LIKE.
                      POLY-ALA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kronstad
             Ustilaginomycetes;
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                                                                                                                                                                                                    CAMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stad J.W.;
fungal pathogen Ustilago
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                                                                                                                                                                                                    synthesis; Magnesium
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        Matches
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Best Local
                                                                                                                                                                                                                                                                                                                01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Glucose-1-phosphate adenylyltransferase small subunit, chloroplast
precursor (EC 2.7.7.27) (ADP-glucose synthase) (ADP-glucose
pyrophosphorylase) (ACPASE B) (Alpha-D-glucose-1-phosphate adenyl
                                                                                                                                                                                                                                                                                                                                                                             Q9M462;
01-MAR-2002
                                                                                                                                                 "Isolation and analysis of a cDNA clone encoding ADP-glucose pyrophosphorylase in the plastids of Oilseed rape (Brassica napus).";
                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=CV. Drakkar; TI
Zawodny S., Martini N.
                                                                                                                                                                                                                                                                                                                                                                                                    GLGS_BRANA
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                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
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                                                                                                                                                                                                                                                                     Brassica napus (Rape).
Eukaryota, Viridiplantae,
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                                                                                                                                                                                                                                                                                                         transferase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHGHTGIARLMLFYARAAAGIVDPAHGTGVANAGLVYFNGRLLAMSEDDLPYQVQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FKKTASLAGSRRGTDDSVDPLTALPPLPGSKSVDEAAANKVDVLQQ-TNNLAQSALVQQ-
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                                                                                                                                                                                                                                             Brassicales; Brassicaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
BELONGS
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Pred. No. 42;
14; Mismatches
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BACTERIAL AND PLANTS GLUCOSE-1-
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No. '
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16-OCT-2001
16-OCT-2001
DNA-binding
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or send a
                   MEDLINE-98204792; PubMed-9535817;
Tanaka N., Ohuchi N., Mukai Y., Osaka Y., Ohtani Y., Tat
Bhuiyan M.S.A., Fukui H., Harashima S., Takegawa K.;
"Isolation and characterization of an invertase and its
genes from Schizosaccharomyces pombe.";
genes from Schizosaccharomyces pombe.";
Biochem. Biophys. Res. Commun. 245:246-253(1998).

1- FUNCTION: INVOLVED IN CARBON CATABOLITE REPRESSION.
THE TRANSCRIPTION OF VARIOUS GENES INCLUDING THE IN

-i- SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ271162; CAB89863.1; ...
Interpro; IPRO(1825; MTP_transferase.
Pfam; PF00483; MTP_transferase; 1.
PROSITE; PS00808; ADP_GLC_PYROPHOSPH_1; 1.
PROSITE; PS00809; ADP_GLC_PYROPHOSPH_2; 1.
PROSITE; PS00810; ADP_GLC_PYROPHOSPH_3; 1.
Glycogen biosynthesis; Transferase; Nucleotidyltransferase;
     <del>-</del> -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCR1_SCHPO
014335;
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TRANSIT
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the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                     Wood V., Rajandream M.A.,
Submitted (AUG-1997) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCRI OR SPECID7.02C.
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4896
                                                                                                                                                                                                                                                                     IDENTIFICATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 TADPSVQIAGNFAPVNEQPVRRNLPVVGKLPDSIKGVYV 154
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mes 43; Conserv
THE TRANSCRII
- SUBCELLULAR I
- SIMILARITY: I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLPRGNERRTPSIVSPKAVSDSQNSQTCLDPDASRSVL----GIILGGGAGTRLYPLTKK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HFPKQSSNSPAIVVKPKA-KESNTKQMNLFQRAAAALDAAEGFLV---SHEKLHPL-PK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MASFTATAAVSGRWLGGNHTQPPLSSSQSSDLSYCSSLPMASRVTRKLNVSSALHTPPAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         520 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein scrl.
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                                                                                                                                                                                                                                                                  AND FUNCTION
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27.0%;
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                                                                                                                                                                                                                                                                                                                                           Barrell B.G., Skelton J., Churcher C.M.;
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  THE CREA/MIG
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Pred. No. 4.7;
27; Mismatches
                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHLOROPLAST (POTENTIAL).
GLUCOSE-1-PHOSPHATE ADENY
SMALL SUBUNIT.
; D0EAFC9706F3B6A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomycetes;
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GROUP
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OF.
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C2H2-TYPE
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                                                    IVV1
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                                                                                REPRESSES
                                                                                                                                                           repressor
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                                                    GENE.
ZINC
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GLGT_VICFA
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Best Local
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                                                                                                                                GLGT_VICFA STAN
P52417;
01-0CT-1996 (Rel. :
01-0CT-1996 (Rel. :
01-MAR-2002 (Rel. :
                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Glucose-1-phosphate adenylyltransferase small subunit 2, chloroplate
precursor (EC 2.7.7.27) (ADP-glucose synthase) (ADP-glucose
precursor-horvlase) (AGPASE B) (Alpha-D-glucose-1-phosphate adenyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Vicia faba (Broad bean).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART: SM00355; ZnF_C2H2; 2

PROSITE; PS00028; ZINC_FINGER_C2H2_2; 2

PROSITE; PS50157; ZINC_FINGER_C2H2_2; DNA-binding; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z98270; CAB10978.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                             AGPP
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                                                                                                                                                                                                                                                                      AHFRYQRRSRPVSPCS-TAPSSPTFSTRSFSP----TPDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATAAVSMSY--PHHYSASVQQQQATFVSNGQPHNLPAQAQPATIYGIPDALHTTQNGTTI 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATAAVSGRWLGGNHTQPPLSSSQSSDLS--YCSSLPMASRVTRKLNVSSALHTP---PAL
                                                                                                                                                                                                                                                                                                  AHPKVDPESGELFALSYDVVSKPYLKYFRFSPDGTKSPDV 335
                                                                                                                                                                                                                                                                                                                                                           GIVDPAHGTGVANAGLVYFNGRLLAMSEDDLPYQVQITPNGDLKTVGRFDFDGQLESTMI 295
                                                                                                                                                                                                                                                                                                                                                                                          FTKYTNGS-----SNSLYSNSSMQTPYLPSKSNSSTSLHSMYGVGT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HVTGTPPGAVSQRSEPDSRLSSMNEMQLLASAAANQLDAA-----PRIT-PT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HFPKQSSNSPAIVVKPKAKESNTKQMNLFQRAAAAALDAAEGFLVSHEKLHPLPKTADPS 120
                                                                                                                                                                                                                                                                                                                                                                                                                    AVKFEHGSASYACRFTQTNRFVQERQLGRPVFP---KAIGELHGHTGIARLMLFYARAAA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQIAGNFAPVNEQP-VRRNLPVVGKLPDSIKGVYVRNGANPLH-EPVTGHHFFDGDGMVH 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSSGVNLMPLSNAPSPPKQMNVVGSLPSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     r protein; Zinc;
G 26 48
G 54 78
G 81 97
509 548
164 167
375 378
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                                                                                                                                                                                             STANDARD;
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78
97
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21.8%;
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C2H2-TYPE.
C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38;
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Pred. No. 5.3;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALA-RICH.
SER-RICH.
POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-SER
                                                                                                                                                                                             PRT;
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                                                                                                                                                                                             512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNTSPNHLASVPNRGLTSNSSTGS
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                                                                                                                     chloroplast
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                  Rosidae;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00809; ADP_GLC_PYROPHOSPH_2; 1.
PROSITE; PS00810; ADP_GLC_PYROPHOSPH_3; 1.
Glycogen biosynthesis; Transferase; Nucleotidyltransferase;
Multigene family; Starch biosynthesis; Allosteric enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00808; PROSITE; PS00809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00483; NTP_transferase; 1. PYROPHOSPH_1; PROSITE; PS00808; ADP_GLC_PYROPHOSPH_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X76941; CAA54260.1; -. InterPro; IPR001825; NTP_transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Planta 195:352-361(1995).
-!- FUNCTION: THIS PROTEIN PLAYS A ROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cell-type specific, coordinate expression of pyrophosphorylase genes in relation to starch seed development of Vicia faba L.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSIT
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         216
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[1]
                                                                    168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Chloroplast (By similarity).

TISSUE SPECIFICITY: LEAVES AND SEEDS.

DEVELOPMENTAL STAGE: IT IS PRESENT IN YOUNG COTYLEDONS AT 14 DAYS AFFER FERTILIZATION (DAF) WHEN CELLS ARE STILL RAPIDLY DIVIDING.

AFFER FERTILIZATION (DAF) WHEN CELLS ARE STILL RAPIDLY DIVIDING.

LEVELS STEADILY ACCUMULATE UNTIL THE END OF THE CELL EXPANSION PHASE (35-40 DAF) AND WITH THE BECINNING OF THE SEEDS DESICCATION PHASE (35-40 DAF) AND WITH THE BECINNING OF THE SEEDS DESICCATION PHASE AT 50 DAF, THE LEVELS DECREASE TO VERY LOW LEVELS.

SIMILARITY: BELONGS TO THE BACTERIAL AND PLANTS GLUCOSE-1-
PHOSPHATE ADENYLYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diphosphate + ADP-glucose.
ENZYME REGULATION: ACTIVATED BY 3'PHOSPHOGLYCERATE,
BY ORTHOPHOSPHATE. ALLOSTERIC REGULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: THIS PROTEIN PLAYS A ROLE IN SYNTHESIS OF SI
IT CATALYSES THE SYNTHESIS OF THE ACTIVATED GLYCOSYL I
ADP-GLUCOSE FROM GLC-1-P AND ATP.
CATALYTIC ACTIVITY: ATP + alpha-b-glucose 1-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATHWAY: STARCH BIOSYNTH SUBUNIT: HETEROTETRAMER.
ELHGHTGIARLMLFYARAAAGIVDPAHGTGVANAGLVYFN--GRLLAMSEDDLPYQVQIT
                                                                                                                                                                                  -----DIPVSNCLNSNISKIYVLTQFN---SASLNRHLSRAYASNLGGYKNEGFVEVLA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLSSSQSSDLSYCSSLPMASRVTRKLNVSSALHTPPALHF-----PKQSSNSPAIVVKP 76
                                                           AQQSPENPNWFQGTADAVRQYLWLFEEHNVLEYLVLAGDHLYRMDYER-----FIQAHR
                                                                                                                                                                                                                                              EQPVRRNLPVVGKLPDSIKGYYVRNGANPLHEPVTGHHF-----FDGDGMVHAVK 181
                                                                                                                                                                                                                                                                                                      KAVSDSKNSQTCLDPDASRSVL----GIILGGGAGTRLYPLTKKRAKPAVPLGANYRLI- 116
                                                                                                                                                                                                                                                                                                                                                                  KA-KESNTKQMNLFQRAAAAALDAAEGFLV---SHEKLHPL-PKTADPSVQIAGNFAPVN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 3.2%; al Similarity 21.0%; 118; Conservative (
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                                                                                                                          -HGSA----SYACRFTQTN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 101;
Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHLOROPLAST (POTENTIAL).
GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE
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RESULT 13
ACVS_EMENI
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P27742;
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PIR; A
                                                                                                      modified
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                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                       "Delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase from Aspergillus nidulans. Molecular characterization of the acvA gene encoding the first enzyme of the penicillin biosynthetic pathway.

J. Biol. Chem. 266:12646-12654(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Delta (L-alpha-aminoadipyl)-L-cysteinyl-D-valine
(EC 6.-.-) (ACV synthetase) (ACVS).
               HSSP; P14687;
                                                                                                                                                 between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
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                                                                                                                                                                                                                                                                                                INTERMEDIATES.
COFACTOR: CONTAINS
                                                                                                                                                                                                                                                                                                                    3101. Chem. 266:12646-12654(1991).
FUNCTION: EACH OF THE CONSTITUENT AMINO ACIDS OF THE TRIPEPTIDE ACV ARE ACTIVATED AS AMINOACYL-ADENYLATES WITH PETTIDE BONDS FORMED THROUGH THE PARTICIPATION OF AMINO ACID THIOLESTER
                                                                                                                                European Bioinformatics Institute.
                                                                                                                                                                                             SIMILARITY: CONTAINS 3 ACYL CARRIER DOMAINS
                                                                                                                                                                                                                         SIMILARITY:
                                                                                                                                                                                                                                                      PATHWAY: FIRST CEPHALOSPORIN.
                                                                                                              SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EMEUropean Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content
                           A40889;
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                                         X54853; CAA38631
                                                                       s requires a license agreement (See an email to license@isb-sib.ch).
                                                                                   non-profit institutions as long and this statement is not removed. requires a license agreement (See
                                                                                                                                                                                                                                       THE N-TERMINUS
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InterPro;

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AMP-bind

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BINDING
ACT_SITE
SEQUENCE
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InterPro; IPR000379; Est_lip_thioest_actsite.
InterPro; IPR001880; phosphopant_attach.
InterPro; IPR001031; Thioesterase.
Pfam; PF00501; AMP-binding; 3.
Pfam; PF00668; Condensation; 3.
Pfam; PF00550; pp-binding; 3.
Pfam; PF00975; Thioesterase; 1.
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DOMAIN
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                                                                                                                                                                                                                                                   ---LVRWIPGSNGEIEYLGRNDFQVKIRGLRIELGEIEAVMSSHPDIKQSVVIAKSGKEG
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                                                                                                                                                                                                   DQKFLVGYFVASSP-----LSPGA-----IRRFMQSRLPGYMIPSSFIPISSLPVTP
                                                                                                                                                                                                                                                                            LPYQVQITP--NGDLKTVGRFDFD-----
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97; Conserv
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39, Created)
39, Last sequence update)
39, Last annotation update)
ior (EC 3.1.3.8) (Phytate 3-phosphatase)
iphate 3-phosphohydrolase).
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DOMAIN 2 (CYSTEIME-ACTIVATING).
DOMAIN 3 (VALINE-ACTIVATING).
ACYL CARRIER (ACP) 1.
ACYL CARRIER (ACP) 2.
ACYL CARRIER (ACP) 3.
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Pred. No. 1.1e+02
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PHOSPHOPANTETHEINE (BY SIMILARITY).
PHOSPHOPANTETHEINE (BY SIMILARITY).
THIOESTERASE (BY SIMILARITY).
MW; CB66B6D232A58CB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3770;
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                   -04W)
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Best Local S
Matches 88
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"Isolation, characterization, molecular gene cloning, and sequencing
of a novel phytase from Bacillus subtilis.";

Appl. Environ. Microbiol. 64:2079-2085(1998).

-i- FUNCTION: CATALYZES THE HYDROLYZIS OF INORGANIC ORTHOPHOSPHATE
FROM PHYTATE. ONLY PHYTATE. ADP, AND ATP WERE HYDROLYZED (100, 75,
AND 50% OF THE RELATIVE ACTIVITY, RESPECTIVELY). HAS MAXIMAL
ACTIVITY AT PH 7 AND 55 DEGREES CELSIUS.

-i- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H(2)0 = D-myo-
inositol 1,2,4,5,6-pentakisphosphate + phosphate.

-i- COTACTOR: ISOLATED ENZYME REQUIRED CALCIUM FOR ITS ACTIVITY AND/OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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between
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Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.

NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
STRAIN-VTT E-68013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (So or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPROUSES, Phytase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98268943; PubMed=9603817;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NHTQPPLSSSQSSDLSYCSSLPMASRVTRKLN-----VSSALHTPPALHFPKQSSNSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is
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VVPDQQVVFKLPEMIRGGSPVVYD----KNK-VARFGILDKYAEDSSNIKWIDAPDCFCFH
                                                    YGRLYIAEEDEA----IWKFSAEPDGGSNGTVIDRADGRHLTRDIEGLTIYYAADGKGYL
                                                                                                 SGELFALSYDVVSKPYLKYFRFSPDGTKSPDVEIQLDQPTMMHDF-----
                                                                                                                                                                                                   GLVYFNGRLLAM---SEDDL-PYQVQITPNGDL--KTVGRFDFDGQLESTMIAHPKVDPE
                                                                                                                                                                                                                                                                                                          RFTQTNRFVQERQLGRPVFP---KAIGELHGHTGIARLMLFYARAAAGIVDPAHGTGVANA
                                                                                                                                                                                                                                                                                                                                                            NVDIRYDFPLNGKKVDIAAASNRSEGKNTIE-----IYAIDGKNGTL----
                                                                                                                                                                                                                                                                                                                                                                                                      EQPVRRNLPVVGKLPDSIKGVYVRNGANPLHEPVTGHHFFDGDGMVHAVKFEHGSASYAC
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                                                                                                                                                                                                                                                     -----QSMTDPDHPIATAINEVYGFT-----LYHSQK--
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383
31922 MW;
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19.3%; Pre
19.3% 71;
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No. 4
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RESULT ATL_STAND IN ATL_STAND I
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P52081;
01-OCT-1996
01-OCT-1996
16-OCT-2001
                          CHAIN
DOMAIN
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Bifunctional autolysin precursor [Includes: N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28); Mannosyl-glycoprotein endo-beta-N-acetylglucosamidase (EC 3.2.1.96)].
                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A Staphylococcus aureus autolysin that has an N-acetylmuramoyl-L-alanine amidase domain and an endo-beta-N-acetylglucosaminidase domain: cloning, sequence analysis, and characterization."; proc. Natl. Acad. Sci. U.S.A. 92:285-289(1995).
                                                                                                         Cell wall;
                                                                                                                                                       Pfam; PF01510; Pfam; PF01832;
                                                                                                                                                                                                       InterPro; IPR002502; Amidase_2.
InterPro; IPR002901; Amidase_4.
                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-1995)
-1- FUNCTION: ENDOHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-NCTC 8325-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus/Staphylococcus group;
NCBI_TaxID=1280;
  DOMAIN
                                                                                SIGNAL
                                                                                                                                    SMART;
                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Foster S.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95116542; PubMed=7816834;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycopeptides.
SUBCELLULAR LOCATION: Secreted.
PIM: UNDERGOES PROTEOLITIC PROCESSING TO GENERATE THE EXTRACELLULAR LYTIC ENZYMES.
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESIDUE REMAINS ATTACHED TO THE PROTEIN; THE REST OF THE OLIGOSACCHARIDE IS RELEASED INTACT.
CATALYTIC ACTIVITY: Hydrolyses the link between N-acetylmuramoyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
FUNCTION: ENDOHYDROLYSIS OF THE DI-N-ACETYLCHITOBIOSYL UNIT :
HIGH-MANNOSE GLYCOPEPTIDES AND GLYCOPROTEINS CONTAINING THE
-[(MAN)5(GLCNAC)2]-ASN STRUCTURE. ONE N-ACETYL-D-GLUCOSAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO FAMILY 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             residues and L-amino acid residues in certain bacterial cell-wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACETYLMURAMOYL-L-ALANINE AMIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LWNAWEEPETDEVVVIGSCMTP--PDSIFNESD-ENL 445
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                                                                                                                                                                                                                                                                D17366; BAA04185.1; -. L41499; AAA99982.1; -.
                                                                                                                                 SM00047; LYZ2;
                                                                                                      Hydrolase;
30
199
776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYDROLASES.
                                                                                                                                                         Amidase_
                                                                                                                                                                                 Amidase_
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775
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                                                                                                      Signal;
                                                                                                                                                         4; 1.
                        ; Multifunctional enzyme; Re
POTENTIAL.
BIFUNCTIONAL AUTOLYSIN.
N-ACETYLMURAMOYL-L-ALANINE
  ENDO-BETA-N-ACETYLGLUCOSAMIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Kohli, Vineet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DO SOFTWARE: WORDERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb storage
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CORRESPONDENCE ADDRESS:
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                                                                                                    105 VSHEKLHPLPKTADPSVQIAGNFAPVNEQPVRRNLP----VVGKLPDSIKGVYVRNGANP 160
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                                                                                                                                                                                                                                                                 TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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                                LH---EPVTGHHFFDGDGMVHAVKFEHGSASYACRFTQTNRFVQE------RQLGRPV 209
FEVGSEPF--YHLFDGQALLHKFDFKEGHVTYHRRFIRTDAYVRAMTEKRIVITEFGTCA 107
                                                                     MSSQVEHP---
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                                                                                                                                       Score 209; DB 1;
Pred. No. 6.1e-13;
9; Mismatches 222
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                                                                                                                                         222;
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RESULT 3
US-08-928-361B-30
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                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF JUNE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
                                                                       NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DC SOFTWARE: PatentIn Release #1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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SEQUENCE CHARACTERISTICS:
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                                    TELEPHONE: 650-324-1677
TELEFAX: 650-324-1678
                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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In Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , CATOLYN, POLYPEPTIDES, GLYCOPROTEINS, PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS, THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES INFECTIONS
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                                                                                               480.76-1(HV)
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; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-928-361B-30
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US-08-700-651-5
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Best Local
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TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum TITLE OF INVENTION: INFECTIONS FILE REFERENCE: 480.19-4(HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER APPLICATION NUMBER: 08/415,751
                                                                                                                             APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUT, JIRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                     GIPVNGGGVVPDEEAKDQADKGKDGLIVPPTNSINKDPVTNTQYSNTTGNIINPETGKV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLPEMIRG-----GSPVVYDKNKVARFGILDKYAEDSSNIKWIDAPDCFCFHLWNAWE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPETDEVVVIGSCMTPPDSIFNESDENLKSVLSEIRLNLKTGESTRRPIISNEDQQVNLE 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -IPGSLPGSLNYPSENTPQQTDE-----ITGKPVDTVTGLPY---------
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; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1721
; TYPE: PRT
; ORGANISM: Cryptosporidium p.
US-08-700-651-5
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                                                                                                                                                      Sequence 6, Application Patent No. 6071518 GENERAL INFORMATION:
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Best Local Similarity
Matches 125; Conserv
                                                                          APPLICANT: Petersen, (
TITLE OF INVENTION: PITITLE OF INVENTION: FITITLE OF INVENTION: SI
                             CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY,
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                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                       NGTSGEQ 1304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHGHTGIARLMLFYARAAAGIVDPAHGTGVAN--AGLVYFNGRL-LAMSEDDLPYQVQIT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -PFNPP-TGH-----LINPTNNNTMDSSFAGAYKYAVSNGIKTDNVYGLPV-----GE
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                385 Sherman
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                                                                          , Carolyn
PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
SPECIES INFECTIONS
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                Avenue,
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                JONES & BIKSA
e, Suite 6
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Pred. No. 0.0044;
5; Mismatches 194;
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Best Local S
Matches 125
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                                                                                                                                                                                                                                                                                                    1032
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APPLICATION NUMBER: US/0
FILING DATE: 12-SEP-1997
                                                                                                                                                                    1122
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TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER US 60/026,062
PAPPLICATION NUMBER US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                 1181 -IPGSLPGSLNYPSFNTPQQTDE-----ITGKPVDTVTGLPY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 30,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                 PNGDLKTVGRFD-----FDGQLESTMIAHPKVDPESGELFALSYDVVSKPYLKYFRFSP 327
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   AGMVNRNMLGRKTKFAYLALAEPWPKVSGFAKV---DLTTGEVKKHLYGDNRYGGEPLFL
                                                                                                                                KLPEMIRG-----GSPVVYDKNKVARFGILDKYAEDSSNIKWIDAPDCFCFHLWNAWE
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                                                                                                                                                                                                                   Query Match
Best Local Similarity 19.99
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INFORMATION FOR SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 650-324-1677
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ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/026,062 FILING DATE: 13-SEP-1996
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   GRPV-
                                  PTTGL----PFNPP-TGH-----LINPTNNNTMDSSFAGAYKYAVSNGIKTDNVY 347
                                                               SIKGVYVRNGANPLHEPVTGHHFFDGDGMVHAVKFEHGSASY--ACRFTQTNRFVQERQL 205
                                                                                                 KIDSISELMYDIESGRLIGQVSKRPIPGS-----IAGDLNPIMKTPTQTD-SVTGKPID 302
                                                                                                                              -FQRAAAAALDAAEGFLVSHEKLHPLPKTADPSVQIAGNFAPVNEQPVRRNLPVVGKLPD 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ID NO:
                                                                                                                                                                                                                             3.7%; Score 116.5; DB 3; 19.9%; Pred. No. 0.0098; ative 74; Mismatches 175;
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PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
THEIR FUNCTIONAL MUTANTS, VARIANTS, AN
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-FPKAIGELHGHTGIARLMLFYARAAAGIVDPAHGTGVAN-- 248
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RESULT 7
US-08-928-361B-5
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                                                                                                                                 ATTONNO.

NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.
TELECOMMUNICATION INFORMATION:
"TRIEPHONE: 650-324-1677
                                                                                       TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
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TITLE OF INVENTION:
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FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
MOLECULE TYPE:
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STATE: CA
                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                   TOPOLOGY:
                                 STRANDEDNESS
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                                                                         CENGTH:
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                                                     amino acid
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PEPTIDES,
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THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
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US-09-461-697-77
; Sequence 77, Applica;
; Patent No. 6277974
; GENERAL INFORMATION:
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                                                          SEQ ID NO 77
                                                                                                                                                                                                                                      APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart I
APPLICANT: Puranam, Kasturi
APPLICANT: Katz, Lawrence C.
                                                                                              CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
                                                                                                                                                           TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: AND TREATING CONDITIONS, TITLE OF INVENTION: CELL DEATH FILE REFERENCE: 10001-005-999
                                                                                                                                                                                                                                                                                                                                           APPLICANT: COGENT NEUROSCIENCE, APPLICANT: Lo, Donald C.
                                                                               SOFTWARE:
ORGANISM: Homo sapiens
                    LENGTH: 412
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSNIKWIDAPDCFCFHLWNAWEEPETDEVVVIGSCMTPPDSIFNESDENLKSVLSEIRLN 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STVSGSTSGSTKP------KPGIPVNGGGVVPDEEAKDQADKGKDGLIVPPTNSINKDP 1276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTNTQYSNTTGNIINPETGKV--IPGSLPGSLNYPSFNTPQQTDE-----ITGKPVDT 1327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGEVKKHLYGDNRYGGEPLFLPGEGGEE
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                                                                           SEQ ID NOS: 466 FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09461697
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RESULT 9
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Best Local Similarity
"hes 74; Conserv
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Patent No. 58012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                      NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD:221
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
                                                                                                                                 FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US SI FILING DATE: 02-0CT-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                APPLICATION NUMBER: US PORTILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: Un
2TP: 77210
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; Sequence 106, Application
; Patent No. 6245331
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                                        SOFTWARE: Pa
SEQ ID NO 106
LENGTH: 741
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 118; Conserv
                                                                                                                                                                                                                APPLICANT: Laal, Suman
APPLICANT: Zolla-Pazner, Susan
APPLICANT: Bellisle, John T
APPLICANT: Bellisle, John T
TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
                                                                                                                               PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1996-12-31
                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/001,984C CURRENT FILING DATE: 1997-12-31
                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2172 amino acid
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
ORGANISM: Mycobacterium tuberculosis
                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1876 FSGGQRDLFEGILQAGXMIVENLRTYKQPAFVYIPKAGELRGGAWVVVDSKI 1927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       537 -EGGEED--EGYI---LCFVHDEKTWKSE--LQIVNAVSLEVEATVKLPSRV 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YSSQMQL---GGPKIMATNGVVHLTVSDDLEGVSAILKWL------SYVPPYVG 1781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYLKYFR--FSPDGTKSPDVEI------QLDQPTMMHDFAITENFVVVPDQQV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIA----RLMLFYARAAAGIVDPAHGTGVANAGLVYFNGRLLAMSEDDLP----YQVQITP 274
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                                                                                       PatentIn Ver. 2.1
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19.9%; Pred. No. 0.65;
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                                                                                                                                                                                                                                                                               Sequence 4, Application US/08097829 Patent No. 5498831 GENERAL IMFORMATION:
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Best Local
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COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                           CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew
ADDRESSEE: Townsend and Townsend Tower, Suite 20
                                                                                                                                                                                                           APPLICANT: Burgess, Diane G.
APPLICANT: Dooner, Hugo K.
TITLE OF INVENTION: Pea ADP-Glucose Pyrophosphorylase
TITLE OF INVENTION: Genes and Their Uses
                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                       CITY: San Francisco
STATE: California
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21.7%;
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Pred. No. 0.47;
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                                               Sequence 4, Application US/08577403
Patent No. 5773693
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Best Local Similarity
GENERAL INFORMATION:
APPLICANT: Burges
APPLICANT: Dooner
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LENGTH: 516 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: ami TOPOLOGY:
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                                                                                                                                                                                         DSSNIKWIDAPDCFCFHLWNAWEEPE----TDEVVVIGSCMTPPDSI 437
                                                                                                                                                                                                                                                                                                     GITKKPVPDFSFYDRSSPIYTQP-----RYLPPSKMLDADITDSVIGEGCVIKNCKIHHS
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFFWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/577,403
FILING DATE: 22-DEC-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/097,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94105
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie
STREET: One Market Plaza, Steuart Tower,
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 516 amino acid
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NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 415-326-2400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
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                              -VVSKP---YLKYFRESPDGTKSPDVEIQLDQPTMMHDFAITENEV----VVPDQQV---
                                                                                                                                                                                                            DHLYRMDYER-----FIQAHRESDADITVASLPMDEARATA-
                                                                                                                                                                                                                                                                             LSRAYASNLGGYKNEGFVEVLAAQQSPENPNWFQGTADAVRQYLWLFEEHNVLEYLVLAG
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GITKKPVPDFSFYDRSSPIYTQP-----RYLPPSKMLDADITDSVIGEGCVIKNCKIHHS
                                                                  LLRDKFPGANDFGSE------VIPGATELGLRVQAYLYDGYWEDIGTIEAFYNANL
                                                                                                     L---KTVGRFDFDGQLESTMIAHPKVDPESGEL----FALSYD---
                                                                                                                                       IDEEGRIVEFSEKPKGEQLKAMKVDTTILGLDDERAKEMPY---IASMGIYVVSKHVMLD
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                                                                                                                                                                                                                                       RFVQERQLGRPVFPKAIGELHGHTGIARLMLFYARAAAGIVDPAHGTGVANAGLVY 253
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Pred. No.
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US-09-335-409-3
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CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 1410
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
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APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
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1015 RHGLRRDLDGKPVVDLTGQDPREAGLDVYARRRSVRTFLEAP 1056
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                                    EM-IR--
                                                                      VGNDAANKLLLAY--VVPEGTRRRAAEQDASLKTERIDARAHAAEADGLSDGERVQFKLA 1014
                                                                                                                                                                                  AMSEDDLPYQVQITPNGDLKTVGRFDFD---
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                                                                                                                                                                                                                                                                                                                                                                     PALMRMLVEHFEGRPDSLARSLRLSL-LSGDWIPVGLPGELQAIRPGVSVISLGGATEAS
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                                  -GGSPVVYDKNKVARFGILDKYAEDSSNIKWIDAP
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23.2%; Pred. No. 2
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RESULT 14 US-09-568-102-3

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US-09-567-969-3
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                                                   GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istval
APPLICANT: Zirkle, Ross
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APPLICANT: Schupp, Thoma:
APPLICANT: Ligon, James
                                                                                                                                             Sequence 3, Application US/09567969 Patent No. 6355457
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Best Local Similarity 23.2%;
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CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cyr, Devon
APPLICANT: GOETIACh, JOETN
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS
FILE REFERENCE: 4-30582A
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CANT: Cyr, Devon
CANT: Goerlach, Joern
OF INVENTION: GENES F
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Zirkle, Ross
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Zirkle, Ross
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 FOR THE BIOSYNTHESIS OF EPOTHILONES
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; Pred. No. 2.4;
57; Mismatches 182; Indels 116;
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; ORGANISM: Sorangium cellulosum
US-09-567-969-3
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Best Local Similarity
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CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
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1015 RHGLRRDLDGKPVVDLTGQDPREAGLDVYARRRSVRTFLEAP 1056
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                                   EM-IR---GGSPVVYDKNKVARFGILDKYAEDSSNIKWIDAP 405
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23.2%;
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Pred. No. 2.
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